

A77N: Ed Hart.

127401

Access DB# \_\_\_\_\_

## SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: Celine Qian Examiner #: 78710 Date: 7/15/04  
 Art Unit: 1636 Phone Number: 272-0777 Serial Number: 09/845064  
 Mail Box and Bldg. Room Location: 2A89/REN Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc. if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: Clean syn. vector. plasmids, 76 plants...

Inventors (please provide full names): Gruber, V. et al.

Earliest Priority Filing Date: 9/3/1999

\*For Sequence Searches Only\* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

*Please search SEQ ID NO: 10 both interference & commercial database.*

## STAFF USE ONLY

Searcher: \_\_\_\_\_

Searcher Phone #: \_\_\_\_\_

Searcher Location: \_\_\_\_\_

Date searched: 7/16/04Date indexed: 7/21/04

Searcher Prep &amp; Review Time: \_\_\_\_\_

Clerical Prep Time: \_\_\_\_\_

Indexing Time: \_\_\_\_\_

## Type of Search

NA Sequence (#) 1

AA Sequence (#) \_\_\_\_\_

Structure (#) \_\_\_\_\_

Bibliographic \_\_\_\_\_

Litigation \_\_\_\_\_

Fulltext \_\_\_\_\_

Patent Family \_\_\_\_\_

Other \_\_\_\_\_

## Vendors and cost where applicable

STN \_\_\_\_\_

Dialog \_\_\_\_\_

Questel Orbit \_\_\_\_\_

OCLink \_\_\_\_\_

Lexis Nexis \_\_\_\_\_

Sequence Systems Q3H

WWW Internet \_\_\_\_\_

Other vendors \_\_\_\_\_

PT 40 112

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# **STIC Search Report**

## **Biotech-Chem Library**

**STIC Database Tracking Number: 127401**

**TO: Celine Qian**  
**Location: REM-2A89/2C70**  
**Art Unit: 1636**  
**Wednesday, July 21, 2004**

**Case Serial Number: 09/845064**

**From: Edward Hart**  
**Location: Biotech-Chem Library**  
**REM-1A55**  
**Phone: 571-272-2512**

**edward.hart@uspto.gov**

### **Search Notes**

Examiner Qian,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

Edward Hart

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# STIC SEARCH RESULTS FEEDBACK FORM

## Biotech-Chem Library

Questions about the scope or the results of the search? Contact *the searcher* or contact:

Mary Hale, Information Branch Supervisor  
571-272-2507 Remsen E01 D86

## Voluntary Results Feedback Form

➤ I am an examiner in Workgroup:  Example: 1610

➤ Relevant prior art **found**, search results used as follows:

- ☐ 102 rejection
- ☐ 103 rejection
- ☐ Cited as being of interest.
- ☐ Helped examiner better understand the invention.
- ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature  
(journal articles, conference proceedings, new product announcements etc.)

➤ Relevant prior art **not found**:

- ☐ Results verified the lack of relevant prior art (helped determine patentability).
- ☐ Results were not useful in determining patentability or understanding the invention.

Comments:

Drop off or send completed forms to STIC/Biotech-Chem Library Remsen Bldg.



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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 20, 2004, 06:57:16 ; Search time 18105 Seconds  
(without alignments)  
11503.081 Million cell updates/sec

Title: US-09-845-064-10  
Perfect score: 4805  
Sequence: 1 cggggtggtgcctcgcc.....gagcgctttggagcgctca 4805

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues  
Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

GenEmbl.\*

- 1: gb.ba.\*
- 2: gb.htg.\*
- 3: gb.in.\*
- 4: gb.om.\*
- 5: gb.ov.\*
- 6: gb.pat.\*
- 7: gb.ph.\*
- 8: gb.pl.\*
- 9: gb.pr.\*
- 10: gb.ro.\*
- 11: gb.sts.\*
- 12: gb.sy.\*
- 13: gb.un.\*
- 14: gb.vi.\*
- 15: em.ba.\*
- 16: em.fun.\*
- 17: em.hum.\*
- 18: em.in.\*
- 19: em.mu.\*
- 20: em.om.\*
- 21: em.or.\*
- 22: em.ov.\*
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- 25: em.pl.\*
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- 31: em.htg.in.\*
- 32: em.htg.other.\*
- 33: em.htg.mus.\*
- 34: em.htg.pln.\*
- 35: em.htg.rod.\*
- 36: em.htg.man.\*
- 37: em.htg.vrt.\*
- 38: em.sy.\*
- 39: em.htgo.hum.\*
- 40: em.htgo.mus.\*
- 41: em.htgo.other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	4805	100.0	4805	6	AX093005	AX093005 Sequence
2	4590.8	95.5	7943	6	AX093010	AX093010 Sequence
3	4549	94.7	10003	6	AX093016	AX093016 Sequence
4	4531.4	94.3	5614	6	AX093011	AX093011 Sequence
5	4531.4	94.3	5971	6	AX092998	AX092998 Sequence
6	4531.4	94.3	6016	6	AX092999	AX092999 Sequence
7	4531.4	94.3	6016	6	AX093001	AX093001 Sequence
8	4531.4	94.3	6017	6	AX093000	AX093000 Sequence
9	4531.4	94.3	6017	6	AX093002	AX093002 Sequence
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17	4531.4	94.3	8987	6	AX093017	AX093017 Sequence
18	4531.4	94.3	9143	6	AX093007	AX093007 Sequence
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25	2880	59.9	3508	6	AX092996	AX092996 Sequence
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ALIGNMENTS

RESULT 1  
AX093005  
LOCUS AX093005  
DEFINITION Sequence 10 from Patent WO0118192.  
ACCESSION AX093005  
VERSION AX093005.1 GI:13509479  
SOURCE .  
KEYWORDS synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
Gruber, V. and Comeau, D.  
AUTHORS Synthetic vectors, transgenic plants containing them, and methods  
TITLE for obtaining them  
JOURNAL Patent: WO 0118192-A 10 15-MAR-2001;

AX093005 4805 bp DNA linear PAT 30-MAR-2001

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rep_origin	655..1263	/note="Origin of replication ori RK2"	
		/note="Origin of replication ori ColEI"	
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misc_feature	4106..4271	/note="TrfA locus from RK2 coding for two proteins, P285 and P382, enabling the increase in the rate of replication"	
		/note="T-DNA left border"	
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misc_feature	4566..4625	/note="MCS multiple cloning site"	
		4625..4798	
misc_feature		/note="T-DNA right border"	
ORIGIN			
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Best Local Similarity		100.0%; Pred. No. 0;	
Matches 4805; Conservative		0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1	CCGGGCTGGTTCCTCGCGCTGGCGCCGCTATGGCCCTGCAACCGCCGAG	60
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Qy	61	AAAGCGCGTTCGAAGCCGTGTCGAGACACCGCGCGCGTGTGGATACCTCCGCG	120
Db	61	AAAGCGCGTTCGAAGCCGTGTCGAGACACCGCGCGCGTGTGGATACCTCCGCG	120
Qy	121	AAAACTTGGCCCTCAGTACAGATGAGGGCGGACGTTGACACTTGAAGGGCCGACTCAC	180
Db	121	AAAACTTGGCCCTCAGTACAGATGAGGGCGGACGTTGACACTTGAAGGGCCGACTCAC	180
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Db	181	CCGGCGGGCGTGTGACAGATGAGGGCGAGGCTCGATTTCCGCGCGGACGTTGGAGCTGGC	240
Qy	241	CAGCCTCGAAAATCGGCGAAAACCCCTGATTTTACGCGAGTTTCCACAGATGATGTGGA	300
Db	241	CAGCCTCGAAAATCGGCGAAAACCCCTGATTTTACGCGAGTTTCCACAGATGATGTGGA	300
Qy	301	CAAGCCTGGGGATAAGTGCCTCGCGTATTGACACTTGAAGGGGCGGACTACTGACAGAT	360
Db	301	CAAGCCTGGGGATAAGTGCCTCGCGTATTGACACTTGAAGGGGCGGACTACTGACAGAT	360
Qy	361	GAGGGCGGATCCTTGACACTTTCAGGGCGAGTGTGACAGATGAGGGCGGACCTAT	420
Db	361	GAGGGCGGATCCTTGACACTTTCAGGGCGAGTGTGACAGATGAGGGCGGACCTAT	420
Qy	421	TGACATTTGAGGGCTGTCCACAGCGCAAAATCCAGCATTTGCAAGGGTTTCGCCCGGT	480
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Db	541	TTTTTAAACGAGGCTGCGCCCTGTGCGGTGACCGCGGACCGCGAGGGGGTCCGCC	600
Qy	601	CTTCTCGAAACCTCCCGGAAAGGTATGCGGTGTGAAATACCGCACAGATGCGTAAGGAGA	660

Db	601	CTTCTCGAACCTCCCGAAAGGTATGCGGTGTGAATACCGCACAGATCGTAAGGAGA	660
Qy	661	AAATACCGCATCAGGGCTCTTCCGCTTCCTCGCTCACTGACTCGCTCGCTGGTCTT	720
Db	661	AAATACCGCATCAGGGCTCTTCCGCTTCCTCGCTCACTGACTCGCTCGCTGGTCTT	720
Qy	721	CGGCTGGGCGAGGGTATCAGCTCACTCAAGCGGTAATACGGTTATCCACAGATCA	780
Db	721	CGGCTGGGCGAGGGTATCAGCTCACTCAAGCGGTAATACGGTTATCCACAGATCA	780
Qy	781	GGGGATAAACCGAGAAAGACATGTGAGCAAAAGGCGAGCAAAAGGCCAGAACCGTAAA	840
Db	781	GGGGATAAACCGAGAAAGACATGTGAGCAAAAGGCGAGCAAAAGGCCAGAACCGTAAA	840
Qy	841	AAGGCGCGTGTGCGGTTTTTCCATAGGCTCCGCCCTTACCGGATACCAAAAAT	900
Db	841	AAGGCGCGTGTGCGGTTTTTCCATAGGCTCCGCCCTTACCGGATACCAAAAAT	900
Qy	901	CGACGCTCAAGTCAGAGGTGGCGAAACCGACAGGACTATAAGATACACGAGGTTTCCC	960
Db	901	CGACGCTCAAGTCAGAGGTGGCGAAACCGACAGGACTATAAGATACACGAGGTTTCCC	960
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Db	1201	CCACTGGCAGACGCTTACCATATATCCCGATTAACCCAGCGAACCATTTGAGGTGAT	1260
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Db	1261	AGGTAGATTTATCCGAGGTATGAAACGAGATTTGACCTTTACAGAACTTCTATGA	1320
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Db	1561	CTTGTAAATTTCAACAAATTTGGTTTCAAAATTCGGCTCCGCTCGATCTATGTTATACG	1620
Qy	1621	CCAACTTTGAAAACAACTTTGAAAAGCTGTTTTCTGGTATTTAAGTTTTAGAAATGCAA	1680
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Qy 1741 GTAGAAAAGAGGAAGAAATAATAATGCGTAAATAGAGTAATATCACCGGAAATGAAAAA 1800  
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Qy 1981 TGTTCCAAAGGTCTGCACTTTGAAACGGCATGATGCTGGAGCAATCTGCTCATGAGTGA 2040  
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ACCESSION AX093010  
VERSION AX093010.1 GI:13509485  
KEYWORDS  
SOURCE synthetic construct

ORGANISM synthetic construct  
REFERENCE 1 artificial sequences.  
AUTHORS Gruber, V. and Comeau, D.  
TITLE Synthetic vectors, transgenic plants containing them, and methods for obtaining them  
JOURNAL Patent: WO 0118192-A 15 15-MAR-2001;  
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4021 CAGTTCGGCTGGGGTTCAGCAGCGCGCTTACTTGGCATTTCTAGGTTGACGCTCTT 4080  
4081 CTGATGGGCTGCTGATCGAGTGGTATTTGTGCGAGCTCCCGTCCGGGAGCTGTT 4140  
4081 CTGATGGGCTGCTGATCGAGTGGTATTTGTGCGAGCTCCCGTCCGGGAGCTGTT 4140  
4141 GGCTGCTGGTGCAGGATATATTTGGTGTAAACAAATGACGCTTAGACACTTAATA 4200  
4141 GGCTGCTGGTGCAGGATATATTTGGTGTAAACAAATGACGCTTAGACACTTAATA 4200  
4201 ACACATTTGGGAGCTTTTAACTACTTGGGCTATCCCGGGGATATCCATAGGCGCG 4260  
4201 ACACATTTGGGAGCTTTTAACTACTTGGGCTATCCCGGGGATATCCATAGGCGCG 4260  
4261 ATCTAGTAAACATAATGACACCGCGCGATATTTATCTTCTAGTTTGGCGCTATTTTG 4320  
4261 ATCTAGTAAACATAATGACACCGCGCGATATTTATCTTCTAGTTTGGCGCTATTTTG 4320  
4321 TTTTCTATCGCGTATTAATGATATAATGCGGACTCTAATCATATAAACCCTCTCAT 4380  
4321 TTTTCTATCGCGTATTAATGATATAATGCGGACTCTAATCATATAAACCCTCTCAT 4380  
4381 AATAACGTCATGATACATGTTAATTTATACATGCTTAACGTAATTAACAGAAATAT 4440  
4381 AATAACGTCATGATACATGTTAATTTATACATGCTTAACGTAATTAACAGAAATAT 4440  
4441 ATGATAATCATCGCAAGACCGGCAACAGGATTCATCTTAAGAAACCTTTATGCAAAATG 4500  
4441 ATGATAATCATCGCAAGACCGGCAACAGGATTCATCTTAAGAAACCTTTATGCAAAATG 4500  
4501 TTTGAACGATCGTTCGAGCTATGGGCGGAGCTTGGCGGCGCTTAACACGCGTGG 4560  
4501 TTTGAACGATCGTTCGAGCTATGGGCGGAGCTTGGCGGCGCTTAACACGCGTGG 4560  
4561 ATCTTAAATTAAGTTCGACTCTAGAGATTCCTC 4594  
4561 ATCTTAAATTAAGTTCGACTCTAGAGATTAATTC 4594

RESULT 3  
AX093016 LOCUS 10003 bp DNA linear PAT 30-MAR-2001  
DEFINITION Sequence 21 from Patent WO0118192.  
ACCESSION AX093016  
VERSION AX093016.1 GI:13509491  
KEYWORDS synthetic construct  
SOURCE



ORGANISM	synthetic construct	artificial sequences.
REFERENCE	1	
AUTHORS	Gruber, V. and Comeau, D.	
TITLE	Synthetic vectors, transgenic plants containing them, and methods for obtaining them	
JOURNAL	Patent: WO 0118192-A 21 15-MAR-2001; MERISTEM THERAPEUTICS (FR)	
FEATURES	Location/Qualifiers	
source	1..10003 /organism="synthetic construct" /mol_type="unassigned DNA" /db_xref="taxon:32630" /note="Plasmid pMRT1210"	
rep_origin	1..654 /note="Origin of replication ori RK2"	
rep_origin	655..1263 /note="Origin of replication ori ColEI"	
misc_feature	1264..2603 /note="NPT III gene coding for neomycin phosphotransferase and Kanamycin resistance"	
misc_feature	2604..4098 /note="TrfA locus from RK2 coding for two proteins, P285 and P382, enabling the increase of the replication rate"	
misc_feature	4106..4271 /note="T-DNA left border"	
terminator	4272..4559 /note="Nopaline synthetase terminator"	
misc_feature	4559..4572 /note="MCS multiple cloning site"	
misc_feature	4594..5169 /note="Bar gene coding for phosphinothricine acetyltransferase and glufosinate resistance"	
intron	5170..5704 /note="Rice Actin Intron"	
promoter	5705..6638 /note="Rice Actin Promoter"	
misc_feature	6646..6672 /note="MCS multiple cloning site"	
promoter	6672..7107 /note="High Molecular Weight Glutenin promoter from wheat"	
misc_feature	7107..7169 /note="MCS multiple cloning site"	
intron	7169..7687 /note="Rice Actin Intron"	
misc_feature	7688..9496 /note="GUS gene coding for beta glucuronidase"	
terminator	9497..9823 /note="Nopaline synthetase terminator"	
misc_feature	9823..9996 /note="T-DNA right border"	
ORIGIN		
Query Match	94.7%;	Score 4549; DB 6; Length 10003;
Best Local Similarity	100.0%;	Pred. No. 0;
Matches 4549; Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
QY	1	CCGGGCTGTTGGCTCCGCTGGGCTGCGGCGCTCTATGGCCCTGCAACGCCGCGAG 60
Db	1	CCGGGCTGTTGGCTCCGCTGGGCTGCGGCGCTCTATGGCCCTGCAACGCCGCGAG 60
QY	61	AAACGCCGTCGAGCCGTGTGCGAGACACCGCGCGCGCGCTGTGGATACCTCGCGG 120
Db	61	AAACGCCGTCGAGCCGTGTGCGAGACACCGCGCGCGCGCTGTGGATACCTCGCGG 120
QY	121	AAAACTTGGCCCTCACTGCACAGATGAGGGCGGACGTTGACCTTGAAGGGGCGGACTCAC 180
Db	121	AAAACTTGGCCCTCACTGCACAGATGAGGGCGGACGTTGACCTTGAAGGGGCGGACTCAC 180
QY	181	CCGGCGCGGCTTGCACAGATGAGGGCGGACGCTCGATTTCCGCGCGGACGTTGAGCTGGC 240
Db	181	CCGGCGCGGCTTGCACAGATGAGGGCGGACGCTCGATTTCCGCGCGGACGTTGAGCTGGC 240

|||||  
Db 1321 AGGCCATATTTAAAGCTTACCMAGACGAAGAGGATCAAGAGGATGAGAGGCGAGATTG 1380  
QY  
1381 CCTTGAATATATTGACAAATCTGATAAGATAAATACATCTTTTATATAGAAGATATCGCCG 1440  
Db 1381 CCTTGAATATATTGACAAATCTGATAAGATAAATACATCTTTTATATAGAAGATATCGCCG 1440  
QY  
1441 TATGTAAGGATTTTCAGGGGCGAAGGCATAGGCAGCGCGCTTATCAATATATCTATAGAAT 1500  
Db 1441 TATGTAAGGATTTTCAGGGGCGAAGGCATAGGCAGCGCGCTTATCAATATATCTATAGAAT 1500  
QY  
1501 GGGCAAGCAATAAAACCTTCGATGGACTTAATGCTTTGAAACCCAGGACAAATAACCTTATAG 1560  
Db 1501 GGGCAAGCAATAAAACCTTCGATGGACTTAATGCTTTGAAACCCAGGACAAATAACCTTATAG 1560  
QY  
1561 CTTGTAAATTTCTACCAAAATTTGTGTTTCAAAATTCGGCTCCGTCGATPACTATGTTATACG 1620  
Db 1561 CTTGTAAATTTCTACCAAAATTTGTGTTTCAAAATTCGGCTCCGTCGATPACTATGTTATACG 1620  
QY  
1621 CCAACTTTGAAACCAACTTTGAAAGAGCTGTTTCTCGTATTTAAAGTTTATAGATGCCAA 1680  
Db 1621 CCAACTTTGAAACCAACTTTGAAAGAGCTGTTTCTCGTATTTAAAGTTTATAGATGCCAA 1680  
QY  
1681 GGAACAGTGAATTTGGAGTTTCTGCTTTGTTATAATTTAGCTTCTTTGGGGTATCTTTAAATACT 1740  
Db 1681 GGAACAGTGAATTTGGAGTTTCTGCTTTGTTATAATTTAGCTTCTTTGGGGTATCTTTAAATACT 1740  
QY  
1741 GTAGAAAAGAGGAAGAAATAATAAATTTGGCTAAATAGAAATATCACCGGAAATGAAAAA 1800  
Db 1741 GTAGAAAAGAGGAAGAAATAATAAATTTGGCTAAATAGAAATATCACCGGAAATGAAAAA 1800  
QY  
1801 ACTGATCGAAAAATACCGCTCGTAAAAGATACGGAAGGAATGTCTCTCTCTAAGGTATTA 1860  
Db 1801 ACTGATCGAAAAATACCGCTCGTAAAAGATACGGAAGGAATGTCTCTCTCTAAGGTATTA 1860  
QY  
1861 TAACTGCTGGGAGAAATGAAAACCTTATTTTAAAAATGACGACACGCGGTATAAAGG 1920  
Db 1861 TAACTGCTGGGAGAAATGAAAACCTTATTTTAAAAATGACGACACGCGGTATAAAGG 1920  
QY  
1921 GACCACCTATGATGTGGAACGGGAAAGGACATGATCTATGCTGGAAGGAAAGCTGCC 1980  
Db 1921 GACCACCTATGATGTGGAACGGGAAAGGACATGATCTATGCTGGAAGGAAAGCTGCC 1980  
QY  
1981 TGTTCGAAAGGCTCTGACATTTGAAACGGCATGATGGCTGGAGCAATCTGCTCATGAGTGA 2040  
Db 1981 TGTTCGAAAGGCTCTGACATTTGAAACGGCATGATGGCTGGAGCAATCTGCTCATGAGTGA 2040  
QY  
2041 GGGCGATGGCGTCTTTGCTCGGAAGAGTATGAAGATGAACAAAGCCCTGAAAAAGATTAT 2100  
Db 2041 GGGCGATGGCGTCTTTGCTCGGAAGAGTATGAAGATGAACAAAGCCCTGAAAAAGATTAT 2100  
QY  
2101 CGAGCTGATGCGGAGTGCAATCAGGCTCTTTTCACTCCATCGACATATCGGATTGTCCTTA 2160  
Db 2101 CGAGCTGATGCGGAGTGCAATCAGGCTCTTTTCACTCCATCGACATATCGGATTGTCCTTA 2160  
QY  
2161 TACGAATAGCTTAGACAGCGCTTAGCGGAATTCGATTAATCTTACTGAATAACGATCTGGC 2220  
Db 2161 TACGAATAGCTTAGACAGCGCTTAGCGGAATTCGATTAATCTTACTGAATAACGATCTGGC 2220  
QY  
2221 CGATGCGATTGCGAAACCTGGGAAGAGACACCTCCATTTAAAGATCCGCGGAGCTGTA 2280  
Db 2221 CGATGCGATTGCGAAACCTGGGAAGAGAGACACCTCCATTTAAAGATCCGCGGAGCTGTA 2280  
QY  
2281 TGAATTTTTTAAAGACGAAAAGCCGGAAGAGAACTTGTCTTTTCCACGCGACCTGGG 2340  
Db 2281 TGAATTTTTTAAAGACGAAAAGCCGGAAGAGAACTTGTCTTTTCCACGCGACCTGGG 2340  
QY  
2341 AGACAGCAACATCTTTTGTGAAGATGCAAGATGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2400  
Db 2341 AGACAGCAACATCTTTTGTGAAGATGCAAGATGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2400  
QY  
2401 CGGCAGGCGGACAAAGTGGTATGACATTTGCTCTCTCGGTCGATCAGGAGGAGTAT 2460  
Db 2401 CGGCAGGCGGACAAAGTGGTATGACATTTGCTCTCTCGGTCGATCAGGAGGAGTAT 2460

2401 CGGCAGGCGGACAAAGTGGTATGACATTTGCTCTCTCGGTCGATCAGGAGGAGTAT 2460  
QY  
2461 CGGGGAAGAACAGTATGTCAGCTATTTTTCATCTTACTTGGGATCAAGCTCTATTGGGA 2520  
Db 2461 CGGGGAAGAACAGTATGTCAGCTATTTTTCATCTTACTTGGGATCAAGCTCTATTGGGA 2520  
QY  
2521 GAAAAATAAATATTTATTTTACTGGATGAATTTGTTTTAGTACTAGATGCTGGCGCAACG 2580  
Db 2521 GAAAAATAAATATTTATTTTACTGGATGAATTTGTTTTAGTACTAGATGCTGGCGCAACG 2580  
QY  
2581 ATGCGCGGCGACAGCAGGAGCGACCGACTTTTCCGCAATCAAGTGTGTTTGGCTCTCAGG 2640  
Db 2581 ATGCGCGGCGACAGCAGGAGCGACCGACTTTTCCGCAATCAAGTGTGTTTGGCTCTCAGG 2640  
QY  
2641 CCAGGCCCAACGCAAGTATTTTGGGCAAGGGGTGCTGTGTTATTCGTGCAAGGCAAGATTC 2700  
Db 2641 CCAGGCCCAACGCAAGTATTTTGGGCAAGGGGTGCTGTGTTATTCGTGCAAGGCAAGATTC 2700  
QY  
2701 GGAATACCAAGTACGAGAAGGACGGCGACAGCGGTCTACGGGACCGACTTTCATTTCCCGATA 2760  
Db 2701 GGAATACCAAGTACGAGAAGGACGGCGACAGCGGTCTACGGGACCGACTTTCATTTCCCGATA 2760  
QY  
2761 AGGTGATTTATCTGGACACCAAGGACACGAGGCGGTCAAATCAGGAATTAAGGCGACATTG 2820  
Db 2761 AGGTGATTTATCTGGACACCAAGGACACGAGGCGGTCAAATCAGGAATTAAGGCGACATTG 2820  
QY  
2821 CCCCGCGGTGAGTTCGGGGCAATCCCAGAGGAGGTGAATGATCGGACGTTTGGACCGGA 2880  
Db 2821 CCCCGCGGTGAGTTCGGGGCAATCCCAGAGGAGGTGAATGATCGGACGTTTGGACCGGA 2880  
QY  
2881 AGGCATACAGGCAAGAACTGATCGACGCGGGGTTTTCCGCGGAGGATGCGAAACCATCG 2940  
Db 2881 AGGCATACAGGCAAGAACTGATCGACGCGGGGTTTTCCGCGGAGGATGCGAAACCATCG 2940  
QY  
2941 CAAAGCGCACCGTTCATGCGTGGCCCGCGGAAACCTTTCCAGTCCGTCGATGCTGTC 3000  
Db 2941 CAAAGCGCACCGTTCATGCGTGGCCCGCGGAAACCTTTCCAGTCCGTCGATGCTGTC 3000  
QY  
3001 AGCAAGCTACGGCAAGATCGAGCGGACAGCGTGAACCTGGCTCCCTCCCTGCGCCCG 3060  
Db 3001 AGCAAGCTACGGCAAGATCGAGCGGACAGCGTGAACCTGGCTCCCTCCCTGCGCCCG 3060  
QY  
3061 CGCATTCGGCGCGCTGGAGCGTTCGCGTCTCGAAACAGGAGGCGGACAGGTTTGGCGGA 3120  
Db 3061 CGCATTCGGCGCGCTGGAGCGTTCGCGTCTCGAAACAGGAGGCGGACAGGTTTGGCGGA 3120  
QY  
3121 AGTCGATACCAATCGACACGCGAGGAACTATGACGACCAAGAGAGGAAACCGCGCGCG 3180  
Db 3121 AGTCGATACCAATCGACACGCGAGGAACTATGACGACCAAGAGAGGAAACCGCGCGCG 3180  
QY  
3181 AGGACCTGGCAAAACAGGTCAGCGGCGCAAGCGGCGCGTTCGCTGAACACACGGAAGC 3240  
Db 3181 AGGACCTGGCAAAACAGGTCAGCGGCGCAAGCGGCGCGTTCGCTGAACACACGGAAGC 3240  
QY  
3241 AGCAGATCAAGGAAATGACAGCTTTCTTGTTCGATATTCGCGCTGGCGCGGACACGATGC 3300  
Db 3241 AGCAGATCAAGGAAATGACAGCTTTCTTGTTCGATATTCGCGCTGGCGCGGACACGATGC 3300  
QY  
3301 GAGCGATGCCAAACGACACGCGCGCTGCTCCCTGTTTCAACGCGGCAACAGAAATTC 3360  
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3361 CGGCGAGGGCGCTGCAAAACAGGTCATTTTCCACGTCACACAGGAGGTCGAAGTACACCT 3420  
Db 3361 CGGCGAGGGCGCTGCAAAACAGGTCATTTTCCACGTCACACAGGAGGTCGAAGTACACCT 3420  
QY  
3421 ACACCGCGCTCGAGCTGCGGGCGGACGATGAACGAACTGGTGTGGCAGCAGGTGAGGT 3480  
Db 3421 ACACCGCGCTCGAGCTGCGGGCGGACGATGAACGAACTGGTGTGGCAGCAGGTGAGGT 3480  
QY  
3481 ACAGCAAGCGCAACCCCTATTCGGCGAGCGGATCACTTTACGTTCTACGAGCTTTGCGAGG 3540  
Db 3481 ACAGCAAGCGCAACCCCTATTCGGCGAGCGGATCACTTTACGTTCTACGAGCTTTGCGAGG 3540

Qy	3541	ACCTGGCTGTCGATCAATGGCCGGTATTACAGAGGCGCGGAAATGCTGTGCGGCC	3600
Db	3541	ACCTGGCTGTCGATCAATGGCCGGTATTACAGAGGCGCGGAAATGCTGTGCGGCC	3600
Qy	3501	TACAGGCGAGCGATGGGCTTACGTCGACCGCGTGGGACCTGGAAATCGGTGCGC	3660
Db	3501	TACAGGCGAGCGATGGGCTTACGTCGACCGCGTGGGACCTGGAAATCGGTGCGC	3660
Qy	3661	TGCTGACCGCTTCCGGTCTCGACCGTGCAGAAAGAGTCCCGTTCAGGCTCTGA	3720
Db	3661	TGCTGACCGCTTCCGGTCTCGACCGTGCAGAAAGAGTCCCGTTCAGGCTCTGA	3720
Qy	3721	TCGACGAGGAAATCGTCTGTCTTCTGCTGCGACCACTACAGAAATTCATATGGGAGA	3780
Db	3721	TCGACGAGGAAATCGTCTGTCTTCTGCTGCGACCACTACAGAAATTCATATGGGAGA	3780
Qy	3781	AGTACCCGAGCTGTCCCGACCGCCGAGATGTCGATTCGATTCAGCTCGACCGGG	3840
Db	3781	AGTACCCGAGCTGTCCCGACCGCCGAGATGTCGATTCGATTCAGCTCGACCGGG	3840
Qy	3841	AGCGTACCCGCTCAAGCTGGAACCTTCCGCTCATGTGCGATCGGATTCACCCGCG	3900
Db	3841	AGCGTACCCGCTCAAGCTGGAACCTTCCGCTCATGTGCGATCGGATTCACCCGCG	3900
Qy	3901	TGAAGAGTGGCGGAGCTGGCGAAGCTTCCGAGAGTTCGAGGCGAGCGGCTGG	3960
Db	3901	TGAAGAGTGGCGGAGCTGGCGAAGCTTCCGAGAGTTCGAGGCGAGCGGCTGG	3960
Qy	3961	TGGAACACGCTGGGTCAATGATGACCTGTGCTGCAACGCTAGGCGCTTGTGGGT	4020
Db	3961	TGGAACACGCTGGGTCAATGATGACCTGTGCTGCAACGCTAGGCGCTTGTGGGT	4020
Qy	4021	CAGTCCGCTGGGTTACGACCGAGCTTCTGCGATTCCTAGCTTACGCTCT	4080
Db	4021	CAGTCCGCTGGGTTACGACCGAGCTTCTGCGATTCCTAGCTTACGCTCT	4080
Qy	4081	CTGATGGCTGCCTGTATCAGTGGTATTTGTCGAGCTGCGGTCGGGAGCTGTT	4140
Db	4081	CTGATGGCTGCCTGTATCAGTGGTATTTGTCGAGCTGCGGTCGGGAGCTGTT	4140
Qy	4141	GGCTGGCTGGGAGATATATGTTGTTGTAACAAATTCAGCTTACGCTTAATA	4200
Db	4141	GGCTGGCTGGGAGATATATGTTGTTGTAACAAATTCAGCTTACGCTTAATA	4200
Qy	4201	ACACATTCGGAGCTTTTATGCTAGCTGGGCTATCCCGGGGATATCCATAGCCCG	4260
Db	4201	ACACATTCGGAGCTTTTATGCTAGCTGGGCTATCCCGGGGATATCCATAGCCCG	4260
Qy	4261	ATCTAGTAACATATGACCGCGCGATATATTTATCTTATCTTATCTTATTTTG	4320
Db	4261	ATCTAGTAACATATGACCGCGCGATATATTTATCTTATCTTATCTTATTTTG	4320
Qy	4321	TTTTCTATCGGTAATTAATGTAATTCGGGACTTAATATATAAAACCCATCTATA	4380
Db	4321	TTTTCTATCGGTAATTAATGTAATTCGGGACTTAATATATAAAACCCATCTATA	4380
Qy	4381	AATAACGTGATGATACATGTTAATTTATACGCTTAACGTTAATCAACAGAAATAT	4440
Db	4381	AATAACGTGATGATACATGTTAATTTATACGCTTAACGTTAATCAACAGAAATAT	4440
Qy	4441	ATGATATATATCGCAAGCGGCAACAGGATTCATCTTAAGAACTTTATTCGCAATG	4500
Db	4441	ATGATATATATCGCAAGCGGCAACAGGATTCATCTTAAGAACTTTATTCGCAATG	4500
Qy	4501	TTTGAACGATCGTTCGAGCTATGGGCCCGAAGCTTGGCCGGCGGTT	4549
Db	4501	TTTGAACGATCGTTCGAGCTATGGGCCCGAAGCTTGGCCGGCGGTT	4549

RESULT 4  
AX093011  
LOCUS

AX093011 5614 bp DNA linear PAT 30-MAR-2001

DEFINITION	Sequence 16 from Patent WO0118192.
ACCESSION	AX093011
VERSION	AX093011.1 GI:13509486
KEYWORDS	synthetic construct
SOURCE	artificial sequences.
ORGANISM	1
REFERENCE	Gruber,V. and Comeau,D.
AUTHORS	Synthetic vectors, transgenic plants containing them, and methods
TITLE	for obtaining them
JOURNAL	Patent: WO 0118192-A 16 15-MAR-2001;
FEATURES	MERISTEM THERAPEUTICS (FR)
source	Location/Qualifiers
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	/note="Plasmid pMRT1202"
rep_origin	1. .654
	/note="Origin of replication ori RK2"
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misc_feature	1264. .2603
	/note="NPT III gene coding for neomycin phosphotransferase
	and kanamycinin resistance"
misc_feature	2604. .4098
	/note="T-tfa locus from RK2 coding for two proteins, P285
	and P382, enabling the increase of the rate of
	replication"
misc_feature	4106. .4271
	/note="T-DNA left border"
terminator	4272. .4559
	/note="Nopaline synthetase terminator"
misc_feature	4575. .5150
	/note="Bar gene coding for phosphinothricin
	acetyltransferase and herbicide resistance"
promoter	5150. .5368
	/note="Nopaline synthetase promoter"
misc_feature	5368. .5434
	/note="MCS multiple cloning site"
misc_feature	5434. .5607
	/note="T-DNA right border"
ORIGIN	
Query Match	94.3%; Score 4531.4; DB 6; Length 5614;
Best Local Similarity	100.0%; Pred. No. 0;
Matches 4532; Conservative	0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	CCGGGCTGGTGGCCCTCGCGCTGGGCTGGCGGCGCTCTATGGCCCTGCAAGCGCCAG	60
Db	1	CCGGGCTGGTGGCCCTCGCGCTGGGCTGGCGGCGCTCTATGGCCCTGCAAGCGCCAG	60
Qy	61	AAACCGGCTCGAAGCGCTGTGGAGACACCGCGGCGCGGCTGTGGATACCTCGCG	120
Db	61	AAACCGGCTCGAAGCGCTGTGGAGACACCGCGGCGCGGCTGTGGATACCTCGCG	120
Qy	121	AAACCTTGGCCCTCACTGACAGATGAGGGCGGACGTTGACACTTGAGGGGCGGACTCAC	180
Db	121	AAACCTTGGCCCTCACTGACAGATGAGGGCGGACGTTGACACTTGAGGGGCGGACTCAC	180
Qy	181	CCGGCGCGGCTTGGAGATGAGGGCGGACGCTCGATTTCGGCGCGGACGCTGGAGCTGGC	240
Db	181	CCGGCGCGGCTTGGAGATGAGGGCGGACGCTCGATTTCGGCGCGGACGCTGGAGCTGGC	240
Qy	241	CAGCCTCGCAAAATCGCGGAAAACGCTGATTTTACCGAGTTTCCACAGATGATGTGA	300
Db	241	CAGCCTCGCAAAATCGCGGAAAACGCTGATTTTACCGAGTTTCCACAGATGATGTGA	300
Qy	301	CAGCCTCGGGGATAGTGCCTCGCGTATTGACACTTGAGGGGCGGACTACTGACAGAT	360
Db	301	CAAGCCTGGGGATAGTGCCTCGCGTATTGACACTTGAGGGGCGGACTACTGACAGAT	360

Qy	361	GAGGGCGGATCCTTGACACTTGAGGGCAGAGTGTGACAGATGAGGGCGGCACCTAT	420
Db	361	GAGGGCGGATCCTTGACACTTGAGGGCAGAGTGTGACAGATGAGGGCGGCACCTAT	420
Qy	421	TGACATTTGAGGGGCTGTCCACAGGCGAAGAAATCCAGCATTTTGCAAGGGTTTCGGCCCGT	480
Db	421	TGACATTTGAGGGGCTGTCCACAGGCGAAGAAATCCAGCATTTTGCAAGGGTTTCGGCCCGT	480
Qy	481	TTTTTGGCCACCGGTAACTGCTCTTTTAACTGCTCTTTTAAACCAATATTTATAAACCTTG	540
Db	481	TTTTTGGCCACCGGTAACTGCTCTTTTAACTGCTCTTTTAAACCAATATTTATAAACCTTG	540
Qy	541	TTTTTAAACAGGCTGCGCCTGTGCGCGTGACCGCGCACCGCGAAGGGGGTGCCCCCC	600
Db	541	TTTTTAAACAGGCTGCGCCTGTGCGCGTGACCGCGCACCGCGAAGGGGGTGCCCCCC	600
Qy	601	CTTCTCGAAACCTCCCGGAAGGTATCGCGTGTGAAATACCGCACAGATCGGTAAGGAGA	660
Db	601	CTTCTCGAAACCTCCCGGAAGGTATCGCGTGTGAAATACCGCACAGATCGGTAAGGAGA	660
Qy	661	AAATACCGCATCAGGCGCTCTTCGGCTTCTCGCTCACTGACTCGCTGCGCTCGGTCGTT	720
Db	661	AAATACCGCATCAGGCGCTCTTCGGCTTCTCGCTCACTGACTCGCTGCGCTCGGTCGTT	720
Qy	721	CGGCTGGCGAGCGGTATCAGCTCACTCAAAGCGGTAAATACGTTTATCCACAGAATCA	780
Db	721	CGGCTGGCGAGCGGTATCAGCTCACTCAAAGCGGTAAATACGTTTATCCACAGAATCA	780
Qy	781	GGGGATAACCGAGAAAGACATGTAGCAAAAGGCCAGCAAAAGGCCAGCAACCGTAAA	840
Db	781	GGGGATAACCGAGAAAGACATGTAGCAAAAGGCCAGCAAAAGGCCAGCAACCGTAAA	840
Qy	841	AAGCGCGGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCAAAAAT	900
Db	841	AAGCGCGGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCAAAAAT	900
Qy	901	CGAGCTCAAGTCAGAGTGCAGAAACCGACAGGACTATAAGATACCAAGCGTTTCCC	960
Db	901	CGAGCTCAAGTCAGAGTGCAGAAACCGACAGGACTATAAGATACCAAGCGTTTCCC	960
Qy	961	CCTGGAAGCTCCCTCGTGGCTCTCTCTGTTCCGACCCCTGCGGCTTACCGGATACCTGTCC	1020
Db	961	CCTGGAAGCTCCCTCGTGGCTCTCTCTGTTCCGACCCCTGCGGCTTACCGGATACCTGTCC	1020
Qy	1021	GCCTTTCTCCCTTCGGGAGCGTGGCGTTTTCTCATAGCTCACGCTGTAGGTATCTCAGT	1080
Db	1021	GCCTTTCTCCCTTCGGGAGCGTGGCGTTTTCTCATAGCTCACGCTGTAGGTATCTCAGT	1080
Qy	1081	TCGGTGTAGTTCGTTCCGCTCCAAAGCTGGGCTGTGACAGAAACCCCGGTTTACGCCCGAC	1140
Db	1081	TCGGTGTAGTTCGTTCCGCTCCAAAGCTGGGCTGTGACAGAAACCCCGGTTTACGCCCGAC	1140
Qy	1141	CGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAAACCCGGTAAGACAGCATTTATCG	1200
Db	1141	CGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAAACCCGGTAAGACAGCATTTATCG	1200
Qy	1201	CCACTGGAGCAGCCTTCTACCAATAATCCGGGATAAACCCAGCGAAACCAATTTAGGTGAT	1260
Db	1201	CCACTGGAGCAGCCTTCTACCAATAATCCGGGATAAACCCAGCGAAACCAATTTAGGTGAT	1260
Qy	1261	AGGTAAGATTATACCGAGGTATGAACCGAAATTTGGACCTTTTACAGAAATTTACTCTATGA	1320
Db	1261	AGGTAAGATTATACCGAGGTATGAACCGAAATTTGGACCTTTTACAGAAATTTACTCTATGA	1320
Qy	1321	AGCGCCATATTTAAAAAGCTACCAAGACGAAAGAGGATGAAGAGGATGAGGAGGAGATTG	1380
Db	1321	AGCGCCATATTTAAAAAGCTACCAAGACGAAAGAGGATGAAGAGGATGAGGAGGAGATTG	1380
Qy	1381	CCTTGAATATATTGACAAATCTGATGAATATACATCTTTTATATAGAAGATATCGCG	1440
Db	1381	CCTTGAATATATTGACAAATCTGATGAATATACATCTTTTATATAGAAGATATCGCG	1440
Qy	1441	TATGTAAGGATTTTCAGGGGGCAAGCATAGGCAGCGGCTTATCAATATATCTATAGAAT	1500

Db	1441	TATGTAAGGATTTTCAGGGGGCAAGCATAGGCAGCGGCTTATCAATATATCTATAGAAT	1500
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ACCESSION AX092998  
VERSION AX092998.1 GI:13509472  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1

AUTHORS Gruber, V. and Comeau, D.  
TITLE Synthetic vectors, transgenic plants containing them, and methods for obtaining them  
JOURNAL Patent: WO 01/8192-A 3 15-MAR-2001;  
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## ORIGIN

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Qy 3481 AGCGAAGCGCACCCCTATTCGCGAGCCGATCACCTTTCACGTTTCTACGAGCTTTGCGAGG 3540  
Db 3481 AGCGAAGCGCACCCCTATTCGCGAGCCGATCACCTTTCACGTTTCTACGAGCTTTGCGAGG 3540  
Qy 3541 ACTGGGCTGGTTCGATCAATTTGCGCGGCTTTACGTCGACCCGAGGAAATGCTCTCGCGCC 3600  
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Qy 3601 TACAGCGAGCGGATGGGCTTTCAGCTCGACCGGCTTGGGCACTGGGATCGGTGTCG 3660  
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Qy 3661 TGTGTCACCGCTTCCGCGTCCCTGAGCCGTCGGAAGAAAAACGTCCTCCCTGCGCAGGTCCTGA 3720  
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Qy 3721 TCGACGAGGAAATTCGCTGCTGCTTTGCTGGCGAACACTACACGAAATTCATATGGGAGA 3780  
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Qy	3781	AGTACCGCAAGCTGTGCGCCGACGGCCCGACGGATGTTTCGACTATTTCAGCTCGCACCGGG	3840
Db	3781	AGTACCGCAAGCTGTGCGCCGACGGCCCGACGGATGTTTCGACTATTTCAGCTCGCACCGGG	3840
Qy	3841	AGCGTACCGCTCAAGCTGGAACCTTCGCGCTCATGTGCGATCGGATTCACACCGCG	3900
Db	3841	AGCGTACCGCTCAAGCTGGAACCTTCGCGCTCATGTGCGATCGGATTCACACCGCG	3900
Qy	3901	TGAAGAAGTGGCGAGCAGGTGGCGAAGCCTGCGAAGAGTTGCGAGGACGGCGCTGG	3960
Db	3901	TGAAGAAGTGGCGAGCAGGTGGCGAAGCCTGCGAAGAGTTGCGAGGACGGCGCTGG	3960
Qy	3961	TGAACAACGCTGGGTCAATGATGACCTGTGTCATTCGCAACGCTAGGGCTTGTGGGT	4020
Db	3961	TGAACAACGCTGGGTCAATGATGACCTGTGTCATTCGCAACGCTAGGGCTTGTGGGT	4020
Qy	4021	CAGTTCGGCTGGGGTTACAGCAGCAGCGCTTACTGGCAATTCCTAGGTTCACGTCCT	4080
Db	4021	CAGTTCGGCTGGGGTTACAGCAGCAGCGCTTACTGGCAATTCCTAGGTTCACGTCCT	4080
Qy	4081	CTGATGGGCTGCCTGTATCGAGTGGTGATTTTGTGCCAGCTGCCGTCGGGAGCTGTT	4140
Db	4081	CTGATGGGCTGCCTGTATCGAGTGGTGATTTTGTGCCAGCTGCCGTCGGGAGCTGTT	4140
Qy	4141	GGCTGGCTGGGAGGATATATTTGTTGTGTAACAAATTCAGCCTTAGCAACTTAATA	4200
Db	4141	GGCTGGCTGGGAGGATATATTTGTTGTGTAACAAATTCAGCCTTAGCAACTTAATA	4200
Qy	4201	ACACATTCGGGACGTTTTTAATGTAATGTTGGGCTATCCCCGGGGATATCATAGGCCCG	4260
Db	4201	ACACATTCGGGACGTTTTTAATGTAATGTTGGGCTATCCCCGGGGATATCATAGGCCCG	4260
Qy	4261	ATCTAGTAACATAATACACCGCGCGGATAATTTATCTAGTTTGGCGCTATATTTTG	4320
Db	4261	ATCTAGTAACATAATACACCGCGCGGATAATTTATCTAGTTTGGCGCTATATTTTG	4320
Qy	4321	TTTCTATCGGTAATTAATGTAATTAATGTTGGGACTCTAATCATATAAAACCCATCTATA	4380
Db	4321	TTTCTATCGGTAATTAATGTAATTAATGTTGGGACTCTAATCATATAAAACCCATCTATA	4380
Qy	4381	AATAACCTCATGCAATTAATGTAATTAATGTTGGGACTCTAATCATATAAAACCCATCTATA	4440
Db	4381	AATAACCTCATGCAATTAATGTAATTAATGTTGGGACTCTAATCATATAAAACCCATCTATA	4440
Qy	4441	ATGATAATCATCGCAAGACCGGCAACAGGATTCATCTTAAGAACTTTATTCGCAATG	4500
Db	4441	ATGATAATCATCGCAAGACCGGCAACAGGATTCATCTTAAGAACTTTATTCGCAATG	4500
Qy	4501	TTTGAACGATCGTTCGTGAGCTATGGCCCGA	4533
Db	4501	TTTGAACGATCGTTCGTGAGCTATGGCCCGA	4533

RESULT 6					
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LOCUS	Sequence 4 from Patent WO0118192.				
DEFINITION	AX02999				
ACCESSION	AX02999.1	GI:13509473			
VERSION					
KEYWORDS	synthetic construct				
SOURCE	synthetic construct				
ORGANISM	artificial sequences.				
REFERENCE	1				
AUTHORS	Gruber, V. and Comeau, D.				
TITLE	Synthetic vectors, transgenic plants containing them, and methods for obtaining them				
JOURNAL	Patent: WO 0118192-A 4 15-MAR-2001;				
MERISTEM	Location/Qualifiers				
FEATURES	1..6016				
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terminator	/note="T-DNA left border"	
terminator	4272..4559	
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promoter	4560..5556	
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ORIGIN

Query Match	94.3%;	Score	4531.4;	DB	6;	Length	6016;
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Gaps	0;						
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Db	1	CCGGGCTGGTTCGCCCTCGCGCTGGGCTGGCGCGCTCTATGGCCCTGCAAAACGCGCCAG	60				
Qy	61	AAACGCGCGTCCGAAGCCGTGTGCGAGACA	CCGCGGCGCGCGCGGCTTGTGGATACCTCGCGG	120			
Db	61	AAACGCGCGTCCGAAGCCGTGTGCGAGACA	CCGCGGCGCGCGCGGCTTGTGGATACCTCGCGG	120			
Qy	121	AAAACCTTGGCCCTCACTGACAGATGAGGGCGGACGTTGACACTTGAGGGGCGGACTCAC	180				
Db	121	AAAACCTTGGCCCTCACTGACAGATGAGGGCGGACGTTGACACTTGAGGGGCGGACTCAC	180				
Qy	181	CCGGCGCGGCGTTGACAGATGAGGGCGGACGCTCGATTTCCGCGCGGCGACGTFGGAGCTGGC	240				
Db	181	CCGGCGCGGCGTTGACAGATGAGGGCGGACGCTCGATTTCCGCGCGGCGACGTFGGAGCTGGC	240				
Qy	241	CAGCCTCGCAAAATCGGCGAAACGCTGATTTTACGCGAGTTTCCACAGATGATGTGGA	300				
Db	241	CAGCCTCGCAAAATCGGCGAAACGCTGATTTTACGCGAGTTTCCACAGATGATGTGGA	300				
Qy	301	CAAGCCTTGGGGATAAGTGCCTCGGCTTATGACACTTGAGGGGCGCGACTACTGACAGAT	360				
Db	301	CAAGCCTTGGGGATAAGTGCCTCGGCTTATGACACTTGAGGGGCGCGACTACTGACAGAT	360				
Qy	361	GAGGGGCGGATCCTTGACACTTGAGGGGCGAGTGTCTGACAGATGAGGGGCGGACCTTAT	420				
Db	361	GAGGGGCGGATCCTTGACACTTGAGGGGCGAGTGTCTGACAGATGAGGGGCGGACCTTAT	420				
Qy	421	TGACATTTGAGGGGCTGTCACAGGCGAGAAAATCCAGCATTTGCAAGGGTTTCCGCGCGGT	480				
Db	421	TGACATTTGAGGGGCTGTCACAGGCGAGAAAATCCAGCATTTGCAAGGGTTTCCGCGCGGT	480				
Qy	481	TTTTTCGGCCACCGCTAAACCTGTCTTTTAACTCTGTTTTTAAACCAATATTTTAAACCTTG	540				
Db	481	TTTTTCGGCCACCGCTAAACCTGTCTTTTAACTCTGTTTTTAAACCAATATTTTAAACCTTG	540				
Qy	541	TTTTTTTAAACAGGGGTGCGCCCTGTGCGGTGACCGCGCACGCGAAGGGGGGTGCGCCGCC	600				
Db	541	TTTTTTTAAACAGGGGTGCGCCCTGTGCGGTGACCGCGCACGCGAAGGGGGGTGCGCCGCC	600				
Qy	601	CTTCTCGAAACCCCTCCCGGAAAGGTATGCGGTGTGAAATACCGCACAGATCGTGAAGAGA	660				



Db 601 |||||CTTCTCGAACCTCCCGGAAGAGTATCGCGTGTGAATATACCGCACAGATCGCTGAAGGAGA 660  
QY 661 AAATACCGCATCAGGCGCTCTCCGCTTCTCGCTCACTGACTCGCTGCGCTCGGTCGTT 720  
Db 661 AAATACCGCATCAGGCGCTCTCCGCTTCTCGCTCACTGACTCGCTGCGCTCGGTCGTT 720  
QY 721 CGGCTCGGCGAGCGGTATCAGCTCACTCAAAGCGGTAATACGGTTATCCACAGAATCA 780  
Db 721 CGGCTCGGCGAGCGGTATCAGCTCACTCAAAGCGGTAATACGGTTATCCACAGAATCA 780  
QY 781 GGGGATAACCGCAGAAAGACATGTGAGCAAAAGGCGCAGCAAAAGGCGCAGGAACCGTAAA 840  
Db 781 GGGGATAACCGCAGAAAGACATGTGAGCAAAAGGCGCAGCAAAAGGCGCAGGAACCGTAAA 840  
QY 841 AAGCGCGGTTGTGCGGTTTTTCCATAGGCTCCGCCCTTCACGAGCATCAAAAAAT 900  
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Db 901 CGACGCTCAAGTCAGAGGTGGGAAACCCGACAGGACTATAAGATACCCAGGCGTTTCCC 960  
QY 961 CTTGGAAGCTCCCTCGTGGCTCTCTGTTTCGACCCCTGCGCTTACCAGGATACCTGTCC 1020  
Db 961 CTTGGAAGCTCCCTCGTGGCTCTCTGTTTCGACCCCTGCGCTTACCAGGATACCTGTCC 1020  
QY 1021 GCCTTCTCCCTTCGGGAAGCGTGGCGCTTCTCATAGCTCAGCTGTAGGTATCTCAGT 1080  
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QY 1081 TCGGTGTAGGTCTGCTCGCTCAAGCTGGTGTGTCAGCAACCCCGCTTCAGCCCGAC 1140  
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QY 1141 CGCTGGCGCTTATCCGGTAACATACGTCTTGAGTCCAAACCCGGTAAGACAGACTTATCG 1200  
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QY 1261 AGTAAGATTATACCGAGGTATGAAACCGAATTCGACTTACAGAAATTAATCTATGA 1320  
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QY 1381 CTTTGAATATTTGACAATACATGAATATACATCTTTTATAGAATATCGCCG 1440  
Db 1381 CTTTGAATATTTGACAATACATGAATATACATCTTTTATAGAATATCGCCG 1440  
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QY 1501 GGGCAAGCATAAAACTTGCAATGGAATGCTTGAATGCTTGAATGCTTGAATGCTTGAAT 1560  
Db 1501 GGGCAAGCATAAAACTTGCAATGGAATGCTTGAATGCTTGAATGCTTGAATGCTTGAAT 1560  
QY 1561 CTTTGAATATTTGCAATGGAATGCTTGAATGCTTGAATGCTTGAATGCTTGAATGCTTGAAT 1620  
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Db 1681 GGAACAGTGAATGGAGTTCTGTTGTTTAAATAGCTTCTTGGGTTATCTTTAAATACT 1740  
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QY 2401 CGGCGAGGCGGACAGATGTGATGACATTTGCCCTTTCGCGTCCGTCGATCAGGGAGATAT 2460  
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Db 2461 CGGGGAAGAACAGTATGTCAGCTATTTTTTTCACCTTACTTGGGGATCAAGCTGATTGGGA 2520  
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Db 2521 GAAAAATAAATATTTATTTTACTGGATGAATTTGTTTGTAGTACCTAGATGTGCGCAACG 2580  
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[illegible]

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Db	3961	TGGAACACGCCCTGGGTCAATGATGACCTGGTGCAATTGCAAAACGCTAGGGCCCTTGTGGGGT	4020
Qy	4021	CAGTTCGGCTGGGGGTTTCAGCAGCCAGCGCTTTACTGCAATTTCTAGGTTGACGTCCT	4080
Db	4021	CAGTTCGGCTGGGGGTTTCAGCAGCCAGCGCTTTACTGCAATTTCTAGGTTGACGTCCT	4080
Qy	4081	CTGATGGGCTGCTGTATCGAGTGGTGATTTTGTGCCGAGCTGCCGCTCGGGAGCTGTT	4140
Db	4081	CTGATGGGCTGCTGTATCGAGTGGTGATTTTGTGCCGAGCTGCCGCTCGGGAGCTGTT	4140
Qy	4141	GGCTGGCTGGTGCCAGGATATATTGTGGTGTAACAAATTTGACGCTTAGACAACTTAAATA	4200
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Qy	4201	ACACATTCGGGACGTTTTTAAATGATCTGGGGCTATCCCGGGGGATATCCATAGGCCCG	4260
Db	4201	ACACATTCGGGACGTTTTTAAATGATCTGGGGCTATCCCGGGGGATATCCATAGGCCCG	4260
Qy	4261	ATCTAGTAACATAATGACACCGCGCGGATATTTTATCCTAGTTTCGGGCTATATTTTG	4320
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Qy	4381	AATAAGCTCATGCAATACATGTTAAATTTATACATGCTTTAAGCTAATTCACAGAAATAT	4440
Db	4381	AATAAGCTCATGCAATACATGTTAAATTTATACATGCTTTAAGCTAATTCACAGAAATAT	4440
Qy	4441	ATGATAATCATCCAGACCGGCAACAGGATTCAAATCTTTAAGAAACTTTTATTCGCAAAATG	4500
Db	4441	ATGATAATCATCCAGACCGGCAACAGGATTCAAATCTTTAAGAAACTTTTATTCGCAAAATG	4500
Qy	4501	TTTGAACGATCGTTTCGTGAGCTATGGGCCGA	4533
Db	4501	TTTGAACGATCGTTTCGTGAGCTATGGGCCGA	4533
RESULT 7			
LOCUS	AX093001	6016 bp	DNA linear PAT 30-MAR-2001
DEFINITION	Sequence 6 from Patent WO0118192.		
ACCESSION	AX093001		
VERSION	AX093001.1	GI:13509475	
KEYWORDS	synthetic construct		
SOURCE	synthetic construct		
ORGANISM	artificial sequences.		
REFERENCE	1		
AUTHORS	Gruber, V. and Comeau, D.		
TITLE	Synthetic vectors, transgenic plants containing them, and methods for obtaining them		
JOURNAL	Patent: WO 0118192-A 6 15-MAR-2001;		
FEATURES	MERISTEM THERAPEUTICS (FR)		
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ORIGIN

Query Match 94.3%; Score 4531.4; DB 6; Length 6016;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 4532; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCGGGCTGGTGGCCCTCGCGCTGGCGCTGGCGCGCTCTATGSCCCTGCAAGCGCCGAG 60  
DB 1 CCGGGCTGGTGGCCCTCGCGCTGGCGCTGGCGCGCTCTATGSCCCTGCAAGCGCCGAG 60

QY 61 AAACGCGCTGCGAAGCCGTGTGCAGACACCGCGCGCGCGCGGCTTGTGGATACCTCGCGG 120  
DB 61 AAACGCGCTGCGAAGCCGTGTGCAGACACCGCGCGCGCGCGGCTTGTGGATACCTCGCGG 120

QY 121 AAAAATTGGCCCTCACTGACAGATGAGGGCGGACGTTGACACTTGAGGGGCGGACTCAC 180  
DB 121 AAAAATTGGCCCTCACTGACAGATGAGGGCGGACGTTGACACTTGAGGGGCGGACTCAC 180

QY 181 CCGGCGCGGCTTGACAGATGAGGGCGAGCTCGATTTCCGCGCGGACGCTGAGAGTGGC 240  
DB 181 CCGGCGCGGCTTGACAGATGAGGGCGAGCTCGATTTCCGCGCGGACGCTGAGAGTGGC 240

QY 241 CAGCCTCGCAATCGCGGAAACCGCTGATTTTACCGGAGTTTCCACAGATGATGTGA 300  
DB 241 CAGCCTCGCAATCGCGGAAACCGCTGATTTTACCGGAGTTTCCACAGATGATGTGA 300

QY 301 CAAGCCTGGGGATAGTGCCCTCGCGTATTGACACTTGAGGGGCGGACTACTGACAGAT 360  
DB 301 CAAGCCTGGGGATAGTGCCCTCGCGTATTGACACTTGAGGGGCGGACTACTGACAGAT 360

QY 361 GAGGGCGCGATCTTGACACTTGAGGGGCGAGTCTGACAGATGAGGGGCGGACTAT 420  
DB 361 GAGGGCGCGATCTTGACACTTGAGGGGCGAGTCTGACAGATGAGGGGCGGACTAT 420

QY 421 TGACATTTGAGGGGCTGCCACAGGCGAGAAATCCAGCATTTTCAAGGGTTTCCGCGCGT 480  
DB 421 TGACATTTGAGGGGCTGCCACAGGCGAGAAATCCAGCATTTTCAAGGGTTTCCGCGCGT 480

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QY 541 TTTTAAACAGGGCTCGGCGCTGTGCGGTGACCGGCGACCGCGAAGGGGGTGCCCGCC 600  
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QY 601 CTTCTCGAACCTCCCGGAAAGGTATGCGGTGGAATACCGACAGATGCGTAAAGGA 660  
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DB 781 GGGGATAACCGCAGGAAAGAACATGTGAGCAAAAGGCGCAGCAAAAGGCGCAGGAACCGTAAA 840  
QY 841 AAGGCGCGCTTGTGCGCTTTTTCATAGGCTCCGCGCCCTGACGAGCATCAAAAAAT 900  
DB 841 AAGGCGCGCTTGTGCGCTTTTTCATAGGCTCCGCGCCCTGACGAGCATCAAAAAAT 900  
QY 901 CGACGCTCAAGTCAGAGTGGCGAAACCGCAGGACTATAAGATACCAAGGCGTTTCCC 960  
DB 901 CGACGCTCAAGTCAGAGTGGCGAAACCGCAGGACTATAAGATACCAAGGCGTTTCCC 960  
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Qy	1921	GACCCTATGATGTGGAACGGGAAAGGACATGATGCTATGCTCGAAGGAAAGCTGCC	1980
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Qy	1981	TGTTCCAAAGGTCTCTGCATTTTGAACGGGCATGATGGCTGGAGCAATCTGCTCATGAGTGA	2040
Dd	1981	TGTTCCAAAGGTCTCTGCATTTTGAACGGGCATGATGGCTGGAGCAATCTGCTCATGAGTGA	2040
Qy	2041	GGCCGATGGCGTCTTTGCTCGGAAGAGTATGAAGATGAACAAAGCCCTGAAAAGATTAT	2100
Dd	2041	GGCCGATGGCGTCTTTGCTCGGAAGAGTATGAAGATGAACAAAGCCCTGAAAAGATTAT	2100
Qy	2101	CGAGCTGATGCGGAGTGATCAGGCTCTTTTCACTCCATCGACATATCGGATTTGCCCTA	2160
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Qy	2221	CGATGTGGATGCGAAMAACTGGGAAGAGAACATCCATTTAAAGATCCGCGCAGCTGTA	2280
Dd	2221	CGATGTGGATGCGAAMAACTGGGAAGAGAACATCCATTTAAAGATCCGCGCAGCTGTA	2280
Qy	2281	TGATTTTTTAAAGACGGAAAGCCCGAAGAGGAACCTTGCTTTTCCACGGCACCTGGG	2340
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Dd	2581	ATGCCGGCGACAGCAGAGGGGACCGACTTCTTCCGATCAAGTGTTTGGCTCTCAGG	2640
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Dd	3781	AGTACCGCAGCTGTCGCGCGCGCGCGGATGTTTCCAGTATTCAGCTCGCACCGGG	3840
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Dd	3841	AGCGGTACCCGCTCAAGCTGGAACCTTCCGCTCATGTGCGGATCGGATTTCCACCGCG	3900
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Dd	3901	TGAAGAGTGGCGGACAGGTGGCGAAGCCTTCGGAAGAGTTGCGAGGACGGCCCTGG	3960
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RESULT 8
AX093000
LOCUS AX093000 6017 bp DNA linear PAT 30-MAR-2001
DEFINITION Sequence 5 from Patent WO0118192.
ACCESSION AX093000
VERSION AX093000.1 GI:13509474
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Gruber, V. and Comeau, D.
TITLE Synthetic vectors, transgenic plants containing them, and methods
for obtaining them
JOURNAL Patent: WO 0118192-A 5 15-MAR-2001;
MERISTEM THERAPEUTICS (FR)
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 4532; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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RESULT 9  
AX093002  
LOCUS AX093002 6017 bp DNA linear PAT 30-MAR-2001  
DEFINITION Sequence 7 from Patent WO0118192.  
ACCESSION AX093002  
VERSION AX093002.1 GI:13509476  
KEYWORDS synthetic construct  
SOURCE synthetic construct  
ORGANISM artificial sequences.  
REFERENCE 1  
AUTHORS Gruber, V. and Comeau, D.  
TITLE Synthetic vectors, transgenic plants containing them, and methods for obtaining them  
JOURNAL Patent: WO 0118192-A 7 15-MAR-2001;  
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5771. .5837  
/note="MCS multiple cloning site"

misc_feature		5837..6010			
ORIGIN		/note="T-DNA right border"			
Query Match		94.3%; Score 4531.4; DB 6; Length 6017;			
Best Local Similarity		100.0%; Pred. No. 0;			
Matches 4532; Conservative		0; Mismatches 1; Indels 0; Gaps 0;			
Qy	1	CCGGGCTGGTGGCCCTCGCGCTGGGCTGGCGGCGGCTGTATGGCCCTGC	60		
Db	1	CCGGGCTGGTGGCCCTCGCGCTGGGCTGGCGGCGGCTGTATGGCCCTGC	60		
Qy	61	AAACGCGCTCGAAGCGGTGTGCAGACACCGCGCGCGCGGCGTGTGGATACCTCGCGG	120		
Db	61	AAACGCGCTCGAAGCGGTGTGCAGACACCGCGCGCGCGGCGTGTGGATACCTCGCGG	120		
Qy	121	AAAACTTGGCCCTCACTGCACAGATGAGGGGCGGACGTTGACACTTGAGGGGCGGACTCAC	180		
Db	121	AAAACTTGGCCCTCACTGCACAGATGAGGGGCGGACGTTGACACTTGAGGGGCGGACTCAC	180		
Qy	181	CGGCGCGCGCTTGACAGATGAGGGGCGGAGCTCGATTTTCGCGCGGCGACGTGAGCTGGC	240		
Db	181	CGGCGCGCGCTTGACAGATGAGGGGCGGAGCTCGATTTTCGCGCGGCGACGTGAGCTGGC	240		
Qy	241	CAGCCTCGCAANTCGGCGAAAACGCTGATTTTACGCGAGTTTCCACAGATGATGGGA	300		
Db	241	CAGCCTCGCAANTCGGCGAAAACGCTGATTTTACGCGAGTTTCCACAGATGATGGGA	300		
Qy	301	CAAGCCTGGGGATAAGTGGCCCTGCGGTATTGACACTTGAGGGGCGGACTACTGACAGAT	360		
Db	301	CAAGCCTGGGGATAAGTGGCCCTGCGGTATTGACACTTGAGGGGCGGACTACTGACAGAT	360		
Qy	361	GAGGGCGGATCCTTGACACTTGAGGGGCGAGTGTGCAGATGAGGGGCGGACCTAT	420		
Db	361	GAGGGCGGATCCTTGACACTTGAGGGGCGAGTGTGCAGATGAGGGGCGGACCTAT	420		
Qy	421	TGACATTTGAGGGCTGTCCACAGGCAGAAAAATCCAGCATTTTGAAGGGTTTCGCGCCGT	480		
Db	421	TGACATTTGAGGGCTGTCCACAGGCAGAAAAATCCAGCATTTTGAAGGGTTTCGCGCCGT	480		
Qy	481	TTTTTCGGCCACCGCTAACCTGTCTTTTAACTGCTTTTAAACCAATATTTATAACCTTG	540		
Db	481	TTTTTCGGCCACCGCTAACCTGTCTTTTAACTGCTTTTAAACCAATATTTATAACCTTG	540		
Qy	541	TTTTTAAACGAGGCTGCGCCCTGTGCGGTGACCGCGACCGCGAAGGGGGTGC CCCCC	600		
Db	541	TTTTTAAACGAGGCTGCGCCCTGTGCGGTGACCGCGACCGCGAAGGGGGTGC CCCCC	600		
Qy	601	CTTCTCGAACCTCCCGAAGGTATGCGGTGTGAATAACCGCACAGATCGGTAAGGGA	660		
Db	601	CTTCTCGAACCTCCCGAAGGTATGCGGTGTGAATAACCGCACAGATCGGTAAGGGA	660		
Qy	661	AAATACCGCATCAGGCGCTCTTCGCTTCTCGCTCACTGACTCGCTCGGCTCGGTCGTT	720		
Db	661	AAATACCGCATCAGGCGCTCTTCGCTTCTCGCTCACTGACTCGCTCGGCTCGGTCGTT	720		
Qy	721	CGGCTCGGCGAGCGGTATCAGCTCACTCAAAGCGGTAAATACGGTTATCCACAGATCA	780		
Db	721	CGGCTCGGCGAGCGGTATCAGCTCACTCAAAGCGGTAAATACGGTTATCCACAGATCA	780		
Qy	781	GGGGATAACGAGAAAGAACATGTAGCAAAAGGCCAGCAAAAGGCCAGGAAACCGTAAA	840		
Db	781	GGGGATAACGAGAAAGAACATGTAGCAAAAGGCCAGCAAAAGGCCAGGAAACCGTAAA	840		
Qy	841	AAGGCGCGTGTGCGGCTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAAT	900		
Db	841	AAGGCGCGTGTGCGGCTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAAT	900		
Qy	901	CGACGCTCAAGTCAGAGTGGCGAAAACCGGACAGACTATAAGATACGAGCGGTTTCCC	960		
Db	901	CGACGCTCAAGTCAGAGTGGCGAAAACCGGACAGACTATAAGATACGAGCGGTTTCCC	960		
Qy	961	CCTGGAAGCTCCCTCGTGGCTCTCCTGTTCCGACCCCTCGCGCTTACCGGATACCTGTGCC	1020		



Db 2041 GGCAGTGGCGTCTTTGCTCGGAAGATGATGAAGTGAACAAAGCCCTGAAAAAGATTAT 2100  
Qy CGAGCTGTATGCGAGTGCATCAGGCTCTTTCACTCCATCGACATATCGGATTGTCCCTA 2160  
Db CGAGCTGTATGCGAGTGCATCAGGCTCTTTCACTCCATCGACATATCGGATTGTCCCTA 2160  
Qy TAGCAATAGCTTATAGACAGCGCTTTAGCCGAATTGGATTACTTACTGAATAACGATCTGGC 2220  
Db TAGCAATAGCTTATAGACAGCGCTTTAGCCGAATTGGATTACTTACTGAATAACGATCTGGC 2220  
Qy CGATGCGATTGCGAAACTGCGAAGAGACATCCCATTTAAAGATCCGCGGAGCTGTA 2280  
Db CGATGCGATTGCGAAACTGCGAAGAGACATCCCATTTAAAGATCCGCGGAGCTGTA 2280  
Qy TGATTTTTTAAAGACGGAAAGCCGGAAGAGAACTTGTCTTTTCCACGGCGACCTGGG 2340  
Db TGATTTTTTAAAGACGGAAAGCCGGAAGAGAACTTGTCTTTTCCACGGCGACCTGGG 2340  
Qy AGACAGCAACATCTTTGTGAAAGATGCGAAAGTAAAGTGGCTTTATTGATCTTGGGAGAAG 2400  
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Qy CGCAGGGCGGACAAAGTGGTATGACATTCGCTTCGCGTCCGATCAGGAGGATAT 2460  
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Qy CGGGGAAGAACAGTATGTCAGCTATTTTGTGATCTTACTGGGATCAAGCTCTGATGGGA 2520  
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Qy GAAATAAAAATATTTATTTACTGGATGAATTTTGTAGTACCTAGATGTGGCGCAACG 2580  
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Db ATGCCGCGCACAGCAGGAGCGCACCGACTTTCTTCGCGATCAAGTGTGTCAGG 2640  
Qy CCAGGCGCCACGCAAGTATTTGGGCAAGGGTGCCTGGTATTCTGTCAGGCAAGATTC 2700  
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Qy GGAATACCAAGTACGAGAAGGACGGCCAGACGGTCTACGGGACCGACTTCATTGCCGATA 2760  
Db GGAATACCAAGTACGAGAAGGACGGCCAGACGGTCTACGGGACCGACTTCATTGCCGATA 2760  
Qy AGGTGGATTATCTGGACACCAAGGACACCGCGGGTCAAAATCAGGAATAAGGGCACATTG 2820  
Db AGGTGGATTATCTGGACACCAAGGACACCGCGGGTCAAAATCAGGAATAAGGGCACATTG 2820  
Qy CCCGCGCTCAGTCGGGGCAATCCCGCAAGGAGGTGAATGAATCGGACGTTTGACCGGA 2880  
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Qy AGCAAGCTACGGCCAGATCGAGCGACAGCTGCAACTGCTCCCTCGCCCTCCCG 3060  
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Qy CGCCATCGGCGCGCTGGAGGTTTCGCTCGTCTCGAAAGGAGCGGACAGGTTTGGCGA 3120  
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Qy AGTCGATGACCATCGACACCGAGGAACATATGACGACCAAGAACCGAAACCGCGCG 3180  
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Qy 3181 AGGACCTGGCAAAACAGGTCAGCGAGGCCAAGCAGGCGCGTTCCTGTAACACACACGAGC 3240  
Db 3181 AGGACCTGGCAAAACAGGTCAGCGAGGCCAAGCAGGCGCGTTCCTGTAACACACACGAGC 3240  
Qy 3241 AGCAGATCAAGGAAATGCAAGCTTTCCTTGTTCGATATTGCGCGTGGCCGGAACGATGC 3300  
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Qy 3301 GAGCGATGCCAAACGACAGCGCCGCTCTGCCCTGTTCCACGCGCAACAAGAAATCC 3360  
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Qy 3361 CGCGCAGGCGCTGCAAAAACAGGTCATTTTCCACGTCAAACAGGACGTAAGATCACCT 3420  
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Qy 3601 TACAGCGCAGCGGATGGGCTTCACTCCGACCGCTTGGGACCTTGGAAATCGGTGTGCG 3660  
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Qy 3781 AGTACCGCAAGCTGTCCGACCGGCTTCCGCTCATGTGCGGATCGGATTCACACCGGG 3840  
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Qy 3961 TGAACAACGCTGGGTCAATGATGACCTGGTGCATTCGAAACGCTAGGGCTTTGGGGT 4020  
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QY 1381 CCTTGAATATATTGACAAATCTGATTAAGATAATACATCTTTTATATAGAAGATATCGCCG|||1440  
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QY 1981 TGTTCCAAAGTCTCGACTTTGAAACGGCATGATGCTGGAGCAATCTGCTCATGATGA|||2040  
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QY 2101 CGAGCTGTATCGGAGTGCATCAGGCTCTTTTCACTCCATCGACATATCGGATTGTCCTTA|||2160

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Db 2581 ATGCGCGGCAAGCAGGAGCGCACCGACTTCTTCCGATCAAGTGTTTTGGCTCTCAGG|||2640  
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QY 3181 AGGACCTGGCAAAACAGGTCAGCGAGGCCAAGCAGGCGCGTGTGTAACACACGAAAGC|||3240  
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Db	1	CCGGGCTGGTTGCCCTCGCCCTGGGCTGGCGCCGCTATGGCCCTGCAAAACGGCCAG	60
Qy	61	AAACCGCGTCGAAGCCGTGTGCGAGACAACGCGGCCGCGCGTGTGGATACCTCGCGG	120
Db	61	AAACCGCGTCGAAGCCGTGTGCGAGACAACGCGGCCGCGCGTGTGGATACCTCGCGG	120
Qy	121	AAAACTTGGCCCTCACTGCACAGATGAGGGGGGAGCTTGACATTTAGGGGGCGACATCAC	180
Db	121	AAAACTTGGCCCTCACTGCACAGATGAGGGGGGAGCTTGACATTTAGGGGGCGACATCAC	180
Qy	181	CCGGCGGGCGTTCACAGATGAGGGGCAGGCTCGATTTTCGGCGCGACGTTGAGCTGGC	240
Db	181	CCGGCGGGCGTTCACAGATGAGGGGCAGGCTCGATTTTCGGCGCGACGTTGAGCTGGC	240
Qy	241	CAGCCTCGCAAAATCGGCGAAACCGCTGATTTACGCGAGTTTCCACACAGATGATGGGA	300
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Qy	301	CAAGCCTGGGGATAAGTGTCCCTGCGGTATTGAACCTTGAGGGGGCGCGACTACGACAGAT	360
Db	301	CAAGCCTGGGGATAAGTGTCCCTGCGGTATTGAACCTTGAGGGGGCGCGACTACGACAGAT	360
Qy	361	GAGGGCGCATCCTTCACACTTGAGGGGCAGAGTGTGACAGATGAGGGGGCGACCTAT	420
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Qy	421	TGACATTTGAGGGCTGTCACAGCGCAGAAAAATCCAGCATTTGCAAGGGTTTCGCCCGT	480
Db	421	TGACATTTGAGGGCTGTCACAGCGCAGAAAAATCCAGCATTTGCAAGGGTTTCGCCCGT	480
Qy	481	TTTTTGGCCACCGCTAACCCTGCTTTTAACTGCTTTTAAACCAATATTTATAAACCCTG	540
Db	481	TTTTTGGCCACCGCTAACCCTGCTTTTAACTGCTTTTAAACCAATATTTATAAACCCTG	540
Qy	541	TTTTTAAACGAGGCTGCGCCTGTGCGGCTGACCGCGCACGCCGAAAGGGGGTCCCCC	600
Db	541	TTTTTAAACGAGGCTGCGCCTGTGCGGCTGACCGCGCACGCCGAAAGGGGGTCCCCC	600
Qy	601	CTTCTCGAAACCTCCCGGAAAGGTATCGGCTGTGAAATACCGCACAGATGCGTAAGGAGA	660
Db	601	CTTCTCGAAACCTCCCGGAAAGGTATCGGCTGTGAAATACCGCACAGATGCGTAAGGAGA	660
Qy	661	AAATACCGCATCAGGCGCTCTTCGCTTCCTCGCTCACTGCTGCTGCTCGTCTGCTT	720
Db	661	AAATACCGCATCAGGCGCTCTTCGCTTCCTCGCTCACTGCTGCTGCTCGTCTGCTT	720
Qy	721	CGGCTGGGGAGCGGTATCAGCTCACTCAAGGCGGTAAATACGGTTATCCACAGATCA	780
Db	721	CGGCTGGGGAGCGGTATCAGCTCACTCAAGGCGGTAAATACGGTTATCCACAGATCA	780
Qy	781	GGGGATAACCGAGAAAGAACATGTGAGCAAAAGCCAGCAAAAGGCCAGAAACCGTAAA	840
Db	781	GGGGATAACCGAGAAAGAACATGTGAGCAAAAGCCAGCAAAAGGCCAGAAACCGTAAA	840
Qy	841	AAGCCCGCTGTGCTGGCGTTTTTCCATAGGCTCGCCCCCTCGACGAGCATCAAAAAT	900
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Qy	901	CGAGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAGAGATACGAGGGTTTCCC	960
Db	901	CGAGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAGAGATACGAGGGTTTCCC	960
Qy	961	CCTGGAGCTCCCTCGTGGCGCTCTCCGTTCGACCCCTGCGCTTACCGGATACCTGTCC	1020
Db	961	CCTGGAGCTCCCTCGTGGCGCTCTCCGTTCGACCCCTGCGCTTACCGGATACCTGTCC	1020
Qy	1021	GCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCAGCGCTGAGGTATCTCAGT	1080
Db	1021	GCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCAGCGCTGAGGTATCTCAGT	1080
Qy	1081	TCGGTGTAGTGTGCTTCGCTCAAAGCTGGGCTGTGTGCAAGAAACCCCGCTTCAGCCGAC	1140

D <sub>b</sub>	T CCGTGTAGGTCGGCTCCAAAGCTGGCGTGTTGTCACGAACCCC CGTTTCACGCCGCAC	1140
Q <sub>y</sub>	C G T G C G C C T T A T C C G G T A A C T A T C G T C H T G A G T C C A A C C C G G T A A G A C A C G A C T T A T C G	1200
D <sub>b</sub>	C G T G C G C C T T A T C C G G T A A C T A T C G T C H T G A G T C C A A C C C G G T A A G A C A C G A C T T A T C G	1200
Q <sub>y</sub>	C A C T G G C A G C A G C C T T C T A C A T A A T C C G C G A T A A A C C A G C G N A C C A I T T G A G G T G A T	1260
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QY	2341	AGACAGCAACATCTTTGTGTGAAAGATGGCAAGTAAAGTGCTTTATTTGATCTTTGGGAGAAG	2400
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VERSION AX093008.1 GI:13509482  
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ACCESSION AX093012
VERSION AX093012.1 GI:13509487
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SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 artificial sequences.
AUTHORS Gruber V. and Coneau D.
TITLE Synthetic vectors, transgenic plants containing them, and methods for obtaining them
JOURNAL Patent: WO 0118192-A 17 15-MAR-2001; MERISTEM THERAPEUTICS (FR)
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Qy	3001	AGCAAGCTACGGCCAAAGTACGAGCGGACGACGCTGCAACTGGCTCCCGCTGCCCTGCCCG	3060
Db	3001	AGCAAGCTACGGCCAAAGTACGAGCGGACGACGCTGCAACTGGCTCCCGCTGCCCTGCCCG	3060
Qy	3061	CGCCATCGGCGCGCTGGAGGTTTGGCTGCTGCTGCAAGAGGAGGCGGAGGTTTGGCGGA	3120
Db	3061	CGCCATCGGCGCGCTGGAGGTTTGGCTGCTGCTGCAAGAGGAGGCGGAGGTTTGGCGGA	3120
Qy	3121	AGTCGATGACCATCGACACCGAGGAATATAGCACCAAGAACGGAAGAACCGCGCGG	3180
Db	3121	AGTCGATGACCATCGACACCGAGGAATATAGCACCAAGAACGGAAGAACCGCGCGG	3180
Qy	3181	AGGACCTGGCAAAACAGGTACGCGAGGCCAAGCAGGCGCGGTTGCTGAAACACACCAAGC	3240
Db	3181	AGGACCTGGCAAAACAGGTACGCGAGGCCAAGCAGGCGCGGTTGCTGAAACACACCAAGC	3240
Qy	3241	AGCAGATCAAGGAATACGACTTTCTTGTTCGATATTCGCGCGTGGCGGACCGATGC	3300
Db	3241	AGCAGATCAAGGAATACGACTTTCTTGTTCGATATTCGCGCGTGGCGGACCGATGC	3300

Qy	3301	GAGCGATGCCAAACGACACGCGCCGCTCTCCCTGTTTCCACGCGCAACAAGAAAATCC	3360
Db	3301	GAGCGATGCCAAACGACACGCGCCGCTCTCCCTGTTTCCACGCGCAACAAGAAAATCC	3360
Qy	3361	CGCGGAGGCGCTGCAAAAACAAGGTCAATTTTCCACGTCAAAGGACGTGAAGATCACCT	3420
Db	3361	CGCGGAGGCGCTGCAAAAACAAGGTCAATTTTCCACGTCAAAGGACGTGAAGATCACCT	3420
Qy	3421	ACACCGCGTCGAGCTGCGGGCGGACGATGACGAACTGGTGTGGCAGCAGGTGTTCAGT	3480
Db	3421	ACACCGCGTCGAGCTGCGGGCGGACGATGACGAACTGGTGTGGCAGCAGGTGTTCAGT	3480
Qy	3481	ACCGAAGCGCACCCCTATCGCGGAGCCGATCACTTTCAGCTTCTACGAGCTTTGCCAGG	3540
Db	3481	ACCGAAGCGCACCCCTATCGCGGAGCCGATCACTTTCAGCTTCTACGAGCTTTGCCAGG	3540
Qy	3541	ACCTGGCTGGTTCGATCAATTCGCGGATTTTACAGAAAGCCGAGGAATGCTGTTCGCGCC	3600
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Qy	3601	TACAGGCGAGCGGATGGGCTTCACTCCGACCGCGTGGGACCTTGGAAATCGGTGTGCG	3660
Db	3601	TACAGGCGAGCGGATGGGCTTCACTCCGACCGCGTGGGACCTTGGAAATCGGTGTGCG	3660
Qy	3661	TGCTGCACCGCTTCCGCGTCTCTGGAACGTCGGCAAGAAACGTCCTCCGTTGCGAGGTCTGA	3720
Db	3661	TGCTGCACCGCTTCCGCGTCTCTGGAACGTCGGCAAGAAACGTCCTCCGTTGCGAGGTCTGA	3720
Qy	3721	TCGACGAGGAAATTCGTCTGCTGTTTGTGGCGACCACTACACGAAATTCATATGGGAGA	3780
Db	3721	TCGACGAGGAAATTCGTCTGCTGTTTGTGGCGACCACTACACGAAATTCATATGGGAGA	3780
Qy	3781	AGTACCGCAGCTGTCCGCGACGGCCGAGGAGTTCGACTATTTTCAGCTCCGACCGGG	3840
Db	3781	AGTACCGCAGCTGTCCGCGACGGCCGAGGAGTTCGACTATTTTCAGCTCCGACCGGG	3840
Qy	3841	AGCGGTACCCGCTCAAGCTGGAAACCTTCGCTCATGTGCGGATCGGATTCACCCCGCG	3900
Db	3841	AGCGGTACCCGCTCAAGCTGGAAACCTTCGCTCATGTGCGGATCGGATTCACCCCGCG	3900
Qy	3901	TGAAGAAGTGGCGAGCAGGTCGGCGAAGCTTCGCAAGAGTTGCGAGGCGAGCGGCTGG	3960
Db	3901	TGAAGAAGTGGCGAGCAGGTCGGCGAAGCTTCGCAAGAGTTGCGAGGCGAGCGGCTGG	3960
Qy	3961	TGGAACAACGCTGGGTCAATGATGACCTGGTGCATTTGCAAAACGCTAGGGCTTTGTGGGT	4020
Db	3961	TGGAACAACGCTGGGTCAATGATGACCTGGTGCATTTGCAAAACGCTAGGGCTTTGTGGGT	4020
Qy	4021	CAGTTCGGCTGGGGTTTCAGCAGCGCGCTTTTACTGGCATTTTCTAGGTTGACGCTTT	4080
Db	4021	CAGTTCGGCTGGGGTTTCAGCAGCGCGCTTTTACTGGCATTTTCTAGGTTGACGCTTT	4080
Qy	4081	CTGATCGGCTCGCTGATCAGTGGTGTATTTGTGCGAGCTCCCGTCCGGGAGCTGTT	4140
Db	4081	CTGATCGGCTCGCTGATCAGTGGTGTATTTGTGCGAGCTCCCGTCCGGGAGCTGTT	4140
Qy	4141	GGCTGCTGGTGGCAGGATATATTGGTGTAAACAAATTCAGCTTAGCAACTTAATA	4200
Db	4141	GGCTGCTGGTGGCAGGATATATTGGTGTAAACAAATTCAGCTTAGCAACTTAATA	4200
Qy	4201	ACACATTGGGAGCTTTTAAATGATCTAGGGGCTATCCCGGGGGATATCCATAGGCGCG	4260
Db	4201	ACACATTGGGAGCTTTTAAATGATCTAGGGGCTATCCCGGGGGATATCCATAGGCGCG	4260
Qy	4261	ATCTAGTAACATAATGACACCGCGCGGATAATTTATCTAGTTTCGCGCTATATTTTG	4320
Db	4261	ATCTAGTAACATAATGACACCGCGCGGATAATTTATCTAGTTTCGCGCTATATTTTG	4320
Qy	4321	TTTTCTATCGCGTATTTAAATGATATATTGGGGACTCTTAATCATATAAAACCCATCTCAT	4380
Db	4321	TTTTCTATCGCGTATTTAAATGATATATTGGGGACTCTTAATCATATAAAACCCATCTCAT	4380

Qy	4381	AATAACGTCAATGCAATTACATGTTAAATTATTACATGCTTAACGTAATTCAACAGAAATTAT	4440
Db	4381	AATAACGTCAATGCAATTACATGTTAAATTATTACATGCTTAACGTAATTCAACAGAAATTAT	4440
Qy	4441	ATGATAATCATCGCAAGACCGGCAACAGGATTCAATCTTAAGAACTTTATTGCCAAATG	4500
Db	4441	ATGATAATCATCGCAAGACCGGCAACAGGATTCAATCTTAAGAACTTTATTGCCAAATG	4500
Qy	4501	TTTGAACGATCGTTTCGTGCGAGCTATGGGCCGA	4533
Db	4501	TTTGAACGATCGTTTCGTGCGAGCTATGGGCCAA	4533
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DEFINITION	Sequence 19 from Patent WO0118192.		
ACCESSION	AX093014		
VERSION	AX093014.1 GI:13509489		
KEYWORDS	synthetic construct		
SOURCE	synthetic construct		
ORGANISM	artificial sequences.		
REFERENCE	1		
AUTHORS	Gruber, V. and Comeau, D.		
TITLE	Synthetic vectors, transgenic plants containing them, and methods for obtaining them		
JOURNAL	Patent: WO 0118192-A 19 15-MAR-2001; MERISTEM THERAPEUTICS (FR)		
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Qy	1	CCGGGCTGGTTGCCCTCGCCGCTGGGCTGGGCGCGCTATGGCCCTGCAACCGCCAG	60
Db	1	CCGGGCTGGTTGCCCTCGCCGCTGGGCTGGGCGCGCTATGGCCCTGCAACCGCCAG	60

Qy	61	AAACGCGCTCGAGCCGTGTGGAGACACCGCGGCGCGCGCGCTTGTGGATACCTCGCG	120
Db	61	AAACGCGCTCGAAGCCGTGTGGAGACACCGCGGCGCGCGCGCTTGTGGATACCTCGCG	120
Qy	121	AAACTTGGCCCTCACTGACAGATGAGGGCGGACGCTTGACACTTGAGGGGCGGACTCAC	180
Db	121	AAACTTGGCCCTCACTGACAGATGAGGGCGGACGCTTGACACTTGAGGGGCGGACTCAC	180
Qy	181	CCGCGCGCGGTTGACAGATGAGGGCGAGCTCGATTTCCGCGCGGACGCTGAGCTGGC	240
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Qy	241	CAGCTCTGCAATCGCGGAAACGCTGATTTACCGGAGTTTCCACAGATGATGGGA	300
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Qy	301	CAAGCCTGGGGATAAGTGGCCCTCGGTAATTGACACTTGAGGGGCGGACTACTGACAGAT	360
Db	301	CAAGCCTGGGGATAAGTGGCCCTCGGTAATTGACACTTGAGGGGCGGACTACTGACAGAT	360
Qy	361	GAGGGCGGATCCTTTGACACTTTGAGGGCGAGTGTGACAGATGAGGGGCGGACTTAT	420
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Qy	421	TGACATTTGAGGGGCTGTCCACAGGCAGAAATCCAGCATTTTCAAGGGTTTCCGCCGT	480
Db	421	TGACATTTGAGGGGCTGTCCACAGGCAGAAATCCAGCATTTTCAAGGGTTTCCGCCGT	480
Qy	481	TTTTCGGCCACCCGCTAACTGTCTTTTAACTCTCTTTTAAACCAATATTTATAAACC	540
Db	481	TTTTCGGCCACCCGCTAACTGTCTTTTAACTCTCTTTTAAACCAATATTTATAAACC	540
Qy	541	TTTTTAACAGGGCTGCGCCCTGTGCGGTGACCGCGACCGCGAAGGGGGTTCGCCCC	600
Db	541	TTTTTAACAGGGCTGCGCCCTGTGCGGTGACCGCGACCGCGAAGGGGGTTCGCCCC	600
Qy	601	CTTCTCGAACCCCTCCCGGAAGGTATGCGGTGTGAATACCGCACAGATCGTAAGGAGA	660
Db	601	CTTCTCGAACCCCTCCCGGAAGGTATGCGGTGTGAATACCGCACAGATCGTAAGGAGA	660
Qy	661	AAATACCGATCAGGGCGCTCTTCCGCTTCTCGCTCACTCACTCGCTCGCTCGCTCGTT	720
Db	661	AAATACCGATCAGGGCGCTCTTCCGCTTCTCGCTCACTCACTCGCTCGCTCGTT	720
Qy	721	CGCTCGCGGACGGGTATCAGCTCACTCAAAGGGGTATACGGTTATCCACAGATCA	780
Db	721	CGCTCGCGGACGGGTATCAGCTCACTCAAAGGGGTATACGGTTATCCACAGATCA	780
Qy	781	GGGGTAACCGCAGGAAGACATGTGAGCAAAAGGCGCAGCAAGGCGGAAACCGTAAA	840
Db	781	GGGGTAACCGCAGGAAGACATGTGAGCAAAAGGCGCAGCAAGGCGGAAACCGTAAA	840
Qy	841	AAGCGCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCGCCCTCGACGAGCATCAAAAAT	900
Db	841	AAGCGCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCGCCCTCGACGAGCATCAAAAAT	900
Qy	901	CGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACAGGGGTTTCCC	960
Db	901	CGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACAGGGGTTTCCC	960
Qy	961	CTTGAAGCTCCCTCGTGGCGCTCTCTCTTCCGACCTCGCGCTTACCGGATACCTGTCC	1020
Db	961	CTTGAAGCTCCCTCGTGGCGCTCTCTCTTCCGACCTCGCGCTTACCGGATACCTGTCC	1020
Qy	1021	GCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGT	1080
Db	1021	GCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGT	1080
Qy	1081	TCGGTGTAGTTCGTTCCGCTCAAGCTGGGCTGTGTGCAAGAACCCCGCTTCAGCCGAC	1140
Db	1081	TCGGTGTAGTTCGTTCCGCTCAAGCTGGGCTGTGTGCAAGAACCCCGCTTCAGCCGAC	1140

QY	1141	CGCTGCGCCCTTATCCGGTAACTATCGTCTTGAFTCCAAACCCGGTAAAGACACGACTTATCG	1200
DB	1141	CGCTGCGCCCTTATCCGGTAACTATCGTCTTGAFTCCAAACCCGGTAAAGACACGACTTATCG	1200
QY	1201	CCACTGGCAGCGCTTCTACCAATATCCGGATTAACCCAGCGAACCATTTCAGGTGAT	1260
DB	1201	CCACTGGCAGCGCTTCTACCAATATCCGGATTAACCCAGCGAACCATTTCAGGTGAT	1260
QY	1261	AGGTAAAGATTATACCGAGGTATGAAACAGAAATGGACCTTTACAGAAATTACTCTATGA	1320
DB	1261	AGGTAAAGATTATACCGAGGTATGAAACAGAAATGGACCTTTACAGAAATTACTCTATGA	1320
QY	1321	AGGCCATATTTAAAAAGCTTACCAAGACGAAGGATGAAGAGGATGAGGAGCAGATTG	1380
DB	1321	AGGCCATATTTAAAAAGCTTACCAAGACGAAGGATGAAGAGGATGAGGAGCAGATTG	1380
QY	1381	CTTTGAATATATTGACAACTACTGATAGATAAATACATCTTTTATATAGAGATATCGCCG	1440
DB	1381	CTTTGAATATATTGACAACTACTGATAGATAAATACATCTTTTATATAGAGATATCGCCG	1440
QY	1441	TATGTAAGGATTTTCAGGGGCAAGGCATAGCGAGCGGCTTATCAATATATCTATAGAAT	1500
DB	1441	TATGTAAGGATTTTCAGGGGCAAGGCATAGCGAGCGGCTTATCAATATATCTATAGAAT	1500
QY	1501	GGCAAAAGCATAAAACTTGCATGGACTAATGCTTGAACCCAGGACAATAACCTTTATAG	1560
DB	1501	GGCAAAAGCATAAAACTTGCATGGACTAATGCTTGAACCCAGGACAATAACCTTTATAG	1560
QY	1561	CTTTGTAATTTCTACCAAAATTTGGTTTCAAAATCGGCTCCGTCGATATCTATGTTATCG	1620
DB	1561	CTTTGTAATTTCTACCAAAATTTGGTTTCAAAATCGGCTCCGTCGATATCTATGTTATCG	1620
QY	1621	CCAACTTTGAAAAACAATTTGAAAAAGCTGTTTTCTGGTATTTAAAGTTTTAGAAATGCAA	1680
DB	1621	CCAACTTTGAAAAACAATTTGAAAAAGCTGTTTTCTGGTATTTAAAGTTTTAGAAATGCAA	1680
QY	1681	GGAACTGTAATTTGGAGTTGCTCTGTTATAATTAGCTTCTGGGGTATCTTTAAATACT	1740
DB	1681	GGAACTGTAATTTGGAGTTGCTCTGTTATAATTAGCTTCTGGGGTATCTTTAAATACT	1740
QY	1741	GTAGAAAAGGAAGGAATAATAATGGCTAAATAGAAATATACCCGGAATTTGAAAAA	1800
DB	1741	GTAGAAAAGGAAGGAATAATAATGGCTAAATAGAAATATACCCGGAATTTGAAAAA	1800
QY	1801	ACTGATCGAAAAATACCGCTGCTTAAAGATACGGAAGGAATCTCTCGCTAAGGTATA	1860
DB	1801	ACTGATCGAAAAATACCGCTGCTTAAAGATACGGAAGGAATCTCTCGCTAAGGTATA	1860
QY	1861	TAAAGCTGGTGGGAGAAAAATGAAAAACCTATATTTAAAAATGACGGACAGCCGGTATAAAG	1920
DB	1861	TAAAGCTGGTGGGAGAAAAATGAAAAACCTATATTTAAAAATGACGGACAGCCGGTATAAAG	1920
QY	1921	GACCACTATGATGTGAACGGGAAAAAGGACATGATGCTATGCTGGAAGGAAAGCTGCC	1980
DB	1921	GACCACTATGATGTGAACGGGAAAAAGGACATGATGCTATGCTGGAAGGAAAGCTGCC	1980
QY	1981	TGTTCCAAAGGCTCTGACCTTTCAACGGCATATGCTGCGAGCAATCTGCTCATGATGA	2040
DB	1981	TGTTCCAAAGGCTCTGACCTTTCAACGGCATATGCTGCGAGCAATCTGCTCATGATGA	2040
QY	2041	GGCCGATGGCGCTCTTTGCTCGGAAGAGATGAAGATGAACAAAGCCCTGAAAAAGATTAT	2100
DB	2041	GGCCGATGGCGCTCTTTGCTCGGAAGAGATGAAGATGAACAAAGCCCTGAAAAAGATTAT	2100
QY	2101	CGAGCTGATGCGGAGTGCAATAGGCTTTTCACTCCATCGACATATCGGATTTGTCCTTA	2160
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QY	2161	TACGAATAGCTTAGACAGCGCTTAGCCGAATTTGGATTACTTACTGAATAACGATCTGGC	2220
DB	2161	TACGAATAGCTTAGACAGCGCTTAGCCGAATTTGGATTACTTACTGAATAACGATCTGGC	2220
QY	2221	CGATGTGGATTGCGAAAACTGGGAAGAAGACACTCCATTTTAAAGATCCGCGGAGCTGTA	2280

DB	2221	CGATGTGGATTGCGAAAACTGGGAAGAAGACACTCCATTTTAAAGATCCGCGGAGCTGTA	2280
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DB	2281	TGATTTTTTAAAGACGGAAAAAGCCGGAAGAACTTGTCTTTTCCACGGCGACCTGGG	2340
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DB	2401	CGGAGGGCGGACAAGTGGTATGA CATTGCTTTCTCGCTCCGCTCCGTCGATCAGGGAGGATAT	2460
QY	2461	CGGGGAAGAACACTATGTCAGCTATTTTTCGACTTCTTACCTTGGGGATCAAGCTGATTGGGA	2520
DB	2461	CGGGGAAGAACACTATGTCAGCTATTTTTCGACTTCTTACCTTGGGGATCAAGCTGATTGGGA	2520
QY	2521	GAAAAATAAATAATATATATTTTACTGGATGAATTTGTTTTAGTACTAGATGTGGCGCAACG	2580
DB	2521	GAAAAATAAATAATATATATTTTACTGGATGAATTTGTTTTAGTACTAGATGTGGCGCAACG	2580
QY	2581	ATGCCGCGCACAAAGCAGGAGCGCACCTTCTTCCGCATCAAGTGTGTTGGCTCTCAGG	2640
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QY	2761	AGGTGGATTATCTGGACACCAAGGACACAGGCGGGTCAAAATCAGGAATTAAGGGCACATTG	2820
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QY	2941	CAAAGCGCACCGTCAATGCGTCCGCGCGCGGAAACCTTCCAGTCCGTCGATGGTCC	3000
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QY	3001	AGCAAGCTACGGCCAAAGATCGAGCGGACAGCGTGCACCTGCTCCCTGCTCCCG	3060
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LOCUS AX093050 8289 bp DNA linear PAT 30-MAR-2001  
DEFINITION Sequence 55 from Patent WO0118192.  
ACCESSION AX093050  
VERSION AX093050.1 GI:13509525  
KEYWORDS .  
SOURCE synthetic construct  
ORGANISM synthetic construct  
artificial sequences.  
REFERENCE 1  
AUTHORS Gruber, V. and Comeau, D.  
TITLE Synthetic vectors, transgenic plants containing them, and methods  
for obtaining them  
JOURNAL Patent: WO 0118192-A 55 15-MAR-2001;  
MERISTEM THERAPEUTICS (FR)  
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Best Local Similarity 100.0%; Pred. No. 0;  
Matches 4532; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Search completed: July 20, 2004, 16:58:01

Job time : 18119 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: July 20, 2004, 07:02:45 ; Search time 1650 Seconds  
(without alignments)

12371.268 Million cell updates/sec

Title: US-09-845-064-10

Perfect score: 4805

Sequence: 1 cgggctgtgctccctgcc.....gagcgcttgcgacgtca 4805

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 segs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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1: Geneseqn1980s.\*

2: Geneseqn1990s.\*

3: Geneseqn2000s.\*

4: Geneseqn2001as.\*

5: Geneseqn2001bs.\*

6: Geneseqn2002s.\*

7: Geneseqn2003as.\*

8: Geneseqn2003bs.\*

9: Geneseqn2003cs.\*

10: Geneseqn2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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28	2536.2	52.8	12093	6	ABQ76791	Abq76791 pUC19 pro
c 29	2536.2	52.8	12241	6	AAQ36732	Ad36732 Binary ve
c 30	2536.2	52.8	12241	6	ABQ73049	Abv73049 Tomato an
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32	2536.2	52.8	13002	6	ABQ76794	Abq76794 pUC19 pro
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ALIGNMENTS

RESULT 1

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AC	AAF80284;	
DT		
DT	29-JUN-2001	(first entry)
XX		
DE	Nucleotide sequence of plasmid pMR1191.	
XX		
KW	Vector; transgenesis; trfA locus; RK2 ori; oriV; P285 protein;	
KW	P382 protein; antibiotic resistance gene; nptIII; transgenic plant; ss.	
XX		
OS	Synthetic.	
XX		
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PF	03-SEP-1999;	
XX		99FR-00011112.



Db 1681 |||||GGACAGTGAATTGGAGTTCGTCTGTATATAATTAGTCTTCTGGGTATCTTTAAATACT1740  
QY 1741 GTAGAAAAGAGGAAGAAAATAATAATGGCTTAAATGAGAAATATCACCGGAAATTGAAAAA1800  
Db 1741 GTAGAAAAGAGGAAGAAAATAATAATGGCTTAAATGAGAAATATCACCGGAAATTGAAAAA1800  
QY 1801 ACTGATCGAAAAATACCGCTGCGTAAAGATACGGAAGGAATGTCTCTCTAAGGTATA1860  
Db 1801 ACTGATCGAAAAATACCGCTGCGTAAAGATACGGAAGGAATGTCTCTCTAAGGTATA1860  
QY 1861 TAAGCTGGTGGGAGAAATGAAACCTATATATTTAAATAATACCGACAGCCGGTATAAAG1920  
Db 1861 TAAGCTGGTGGGAGAAATGAAACCTATATTTAAATAATACCGACAGCCGGTATAAAG1920  
QY 1921 GACCACCTATGATGTGAAACGGGAAAGGACATGATCTATGCTGGAAGGAAAGCTGCC1980  
Db 1921 GACCACCTATGATGTGAAACGGGAAAGGACATGATCTATGCTGGAAGGAAAGCTGCC1980  
QY 1981 TGTTCCAAAGGTCTGCACTTTGAAACGGCATGATGGCTGGAGCAATCTGCTCATGAGTGA2040  
Db 1981 TGTTCCAAAGGTCTGCACTTTGAAACGGCATGATGGCTGGAGCAATCTGCTCATGAGTGA2040  
QY 2041 GCGCGATGGCGTCTTGTCTCGGAAGAGTATGAAGTGAACAAAGCCCTGAAAGAGATTAT2100  
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QY 2101 CGAGCTGTATGCGGAGTGCAATCAGGCTCTTTCACTCCATCGACATATCGGATTTGCCCTA2160  
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QY 2161 TACGAATAGCTTACAGACCGCTTACCGAATTTGGAATTACTTACTGAATAACGATCTGGC2220  
Db 2161 TACGAATAGCTTACAGACCGCTTACCGAATTTGGAATTACTTACTGAATAACGATCTGGC2220  
QY 2221 CGATGTGGATGCGAAAACTGGGAAGAGACACTCCATTTAAAGATCCGCGCAGCTGTGA2280  
Db 2221 CGATGTGGATGCGAAAACTGGGAAGAGACACTCCATTTAAAGATCCGCGCAGCTGTGA2280  
QY 2281 TGATTTTTTAAAGACGGAAAGCCCGAAGAGAACTTGTCTTTTCCACGGCACCTGGG2340  
Db 2281 TGATTTTTTAAAGACGGAAAGCCCGAAGAGAACTTGTCTTTTCCACGGCACCTGGG2340  
QY 2341 AGACAGCAACATCTTTGTGAAAGATGCGAAAGTAAAGTGGCTTTATTGATCTTGGGAGAAG2400  
Db 2341 AGACAGCAACATCTTTGTGAAAGATGCGAAAGTAAAGTGGCTTTATTGATCTTGGGAGAAG2400  
QY 2401 CGGACGGCGGACAAGTGGTATGACATTTGCTCTTCTGCGTCCGATCAGGAGGATAT2460  
Db 2401 CGGACGGCGGACAAGTGGTATGACATTTGCTCTTCTGCGTCCGATCAGGAGGATAT2460  
QY 2461 CCGGGAGAACAGTATGTCAGCTATTTTGTAGCTTACTGGGATCAAGCTCATTTGGGA2520  
Db 2461 CCGGGAGAACAGTATGTCAGCTATTTTGTAGCTTACTGGGATCAAGCTCATTTGGGA2520  
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Db 2521 GAAAAATAAATAATATATTTTCTGGAATGAAATTTTGTAGTACTAGATGTGGCGCAACG2580  
QY 2581 ATCCCGCGCAACAGAGGAGCGCACCGACTTCTTCGCAATCAAGTGTGTTGGCTCTCAGG2640  
Db 2581 ATCCCGCGCAACAGAGGAGCGCACCGACTTCTTCGCAATCAAGTGTGTTGGCTCTCAGG2640  
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Db 2641 CCGAGGCCCAACAGTATTTTGGGCAAGGGGTGCTGTTTCTGTCAGGCGCAAGATTTC2700  
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QY 2761 AGGTGGAATTATCTGGGACACCAAGGCAACGAGCGGGTCAATCAGGAATAAGGGCAATTG2820  
Db 2820 |||||

Db 2761 AGGTGGAATTATCTGGGACACCAAGGCAACGAGCGGGTCAAAATCAGGAATAAGGGCAATTG2820  
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Db 2821 CCCCAGCGTGAAGTGGGGCAATCCCGCAAGGAGGGTGAATGAATCGGACGTTTTGACCGGA2880  
QY 2881 AGGCATACAGGCAAGAACTGATCGACGCGGGGTTTTCCGCCGAGGATGCGCAAAACCATCG2940  
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QY 3001 AGCAAGTACGGCAAGATCGAGCGGACAGCGCTGCAACTGGCTCCCCCTGCCCTGCGCCG3060  
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QY 3241 AGCAGATCAAGGAAATGCGAGCTTTCCTTGTTCGATATTGGCGCTGGCGGACACGATGC3300  
Db 3241 AGCAGATCAAGGAAATGCGAGCTTTCCTTGTTCGATATTGGCGCTGGCGGACACGATGC3300  
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Db 3301 GAGCGATGCCAAACGACACGCGCCGCTCTGCCCTGTTTCAACGCGCGCAACAAAGAAATCC3360  
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QY 3421 ACACCGCGCTCGAGCTGCGGGCGGACGATGACGAACTGGTGTGGCAGCAGGTGTTGAGT3480  
Db 3421 ACACCGCGCTCGAGCTGCGGGCGGACGATGACGAACTGGTGTGGCAGCAGGTGTTGAGT3480  
QY 3481 ACGGAAGCGCACCCCTATCGGGAGCGCATCACTTCACTTCACTTCACTTCACTTCACTT3540  
Db 3481 ACGGAAGCGCACCCCTATCGGGAGCGCATCACTTCACTTCACTTCACTTCACTTCACTT3540  
QY 3541 ACCTGGCTGGTTCGATCAATGCGCGGTATTACACGAAGCGCGAGGAATGCTCTGTCGCGCC3600  
Db 3541 ACCTGGCTGGTTCGATCAATGCGCGGTATTACACGAAGCGCGAGGAATGCTCTGTCGCGCC3600  
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Db 3601 TACAGCGCAGCGCGATGGGCTTCACTCCGACCGCGTGGGCACTTGGAACTCGGTGTGCG3660  
QY 3661 TGTGTCAACCGCTTCCGCGTCTGGACCGGTGGCAAGAAACGTCCTGTCAGGCTTCCAGTCTGA3720  
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QY 3721 TCGACGAGGAAATCGCTGCTGTTTGTCTGGCGACCACTACAGAAATTCATATGGGAGA3780  
Db 3721 TCGACGAGGAAATCGCTGCTGTTTGTCTGGCGACCACTACAGAAATTCATATGGGAGA3780  
QY 3781 AGTACCGCAAGCTGTGCGCGACGGCCCGGACGGATGTTTCGACTATTTTTCAGTCTCGACCGGG3840  
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QY 3841 AGCCGTACCCGCTCAAGCTGGAAAACCTTCCGCTCATGTGCGGATCGGATTTCCACCGCG3900  
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Qy 3901 TGAAGAAGTGGCGGACAGCGTGGCGAAGCTGCGAAGAGTTGCGAGGAGCGGCGCTGG 3960  
Dd 3901 TGAAGAAGTGGCGGACAGCGTGGCGAAGCTGCGAAGAGTTGCGAGGAGCGGCGCTGG 3960  
Qy 3961 TGAACACGCGTGGCTCAATGATGACCTGGTGCATTGCAAAAGCTAGGGCTTGTGGGT 4020  
Dd 3961 TGAACACGCGTGGCTCAATGATGACCTGGTGCATTGCAAAAGCTAGGGCTTGTGGGT 4020  
Qy 4021 CAGTTCGGCTGGGGGTTACGACGCCAGCGCTTTACTGGCATTTCTTAGGTGACGCTTT 4080  
Dd 4021 CAGTTCGGCTGGGGGTTACGACGCCAGCGCTTTACTGGCATTTCTTAGGTGACGCTTT 4080  
Qy 4081 CTGATGGGCTGCCTGTATCAGATGGTGATTTTGTGCGAGCTGCGCGTGGGAGCTGTT 4140  
Dd 4081 CTGATGGGCTGCCTGTATCAGATGGTGATTTTGTGCGAGCTGCGCGTGGGAGCTGTT 4140  
Qy 4141 GGCTGGCTGGGAGGATATATTGCTGTAAACAAATTCAGCTTAGACAACTTAATA 4200  
Dd 4141 GGCTGGCTGGGAGGATATATTGCTGTAAACAAATTCAGCTTAGACAACTTAATA 4200  
Qy 4201 ACACATTGCGGACGTTTTTAAATGTAAGTGGGCTATCCCGGGGATATCATAGGCCG 4260  
Dd 4201 ACACATTGCGGACGTTTTTAAATGTAAGTGGGCTATCCCGGGGATATCATAGGCCG 4260  
Qy 4261 ATCTAGTAACATATGACACGCGCGGATTAATTTATCTAGTTTGGCGGTATATTTG 4320  
Dd 4261 ATCTAGTAACATATGACACGCGCGGATTAATTTATCTAGTTTGGCGGTATATTTG 4320  
Qy 4321 TTTTCTATCGGTATTAATGTAATTTGCGGACTCTAATCATATAAAACCCATCTCATA 4380  
Dd 4321 TTTTCTATCGGTATTAATGTAATTTGCGGACTCTAATCATATAAAACCCATCTCATA 4380  
Qy 4381 AATAACGTCATGCAATTAATGTAATTTATCATGCTTAAGCTAATTAACAGAAATAT 4440  
Dd 4381 AATAACGTCATGCAATTAATGTAATTTATCATGCTTAAGCTAATTAACAGAAATAT 4440  
Qy 4441 ATGATAATCATCGCAAGACGCGCAAGGATTAATCTTAAGAACTTTATGCGCAATG 4500  
Dd 4441 ATGATAATCATCGCAAGACGCGCAAGGATTAATCTTAAGAACTTTATGCGCAATG 4500  
Qy 4501 TTTGAAAGATCGTTGCTGAGCTATGGCCCGAAGCTTGGCGGCGTTAACACGCGTGG 4560  
Dd 4501 TTTGAAAGATCGTTGCTGAGCTATGGCCCGAAGCTTGGCGGCGTTAACACGCGTGG 4560  
Qy 4561 ATCCTTAATTAAGTCTAGACTCTAGAGAATTCACTCGAGCAGATTGCTGTTCCCGCTTCA 4620  
Dd 4561 ATCCTTAATTAAGTCTAGACTCTAGAGAATTCACTCGAGCAGATTGCTGTTCCCGCTTCA 4620  
Qy 4621 GTTTAAACTATCAGTGTTCGACGAGTATATGCGGGTAAACCTAAGAGAAAGAGCGT 4680  
Dd 4621 GTTTAAACTATCAGTGTTCGACGAGTATATGCGGGTAAACCTAAGAGAAAGAGCGT 4680  
Qy 4681 TTATTAGAATAATCGGATATTTAAAGGGCGTAAAGGTTTATCCGTTGCTCCATTTGT 4740  
Dd 4681 TTATTAGAATAATCGGATATTTAAAGGGCGTAAAGGTTTATCCGTTGCTCCATTTGT 4740  
Qy 4741 ATGTGATGCCAACACAGGGTTTTACCGGTTTCTTAGGAAAGACCGAGCGCTTTGGAC 4800  
Dd 4741 ATGTGATGCCAACACAGGGTTTTACCGGTTTCTTAGGAAAGACCGAGCGCTTTGGAC 4800  
Qy 4801 GCTCA 4805  
Dd 4801 GCTCA 4805

RESULT 2  
ID AAF80289 standard; DNA; 7943 BP.  
XX AC  
XX AAF80289;  
XX DT 29-JUN-2001 (first entry)

XX Nucleotide sequence of plasmid pMRT1201.  
DE Vector; transgenesis; trfA locus; RK2 ori; oriV; P285 protein;  
XX P382 protein; antibiotic resistance gene; nptIII; transgenic plant; ss.  
KW Synthetic.  
OS  
XX  
FH Key Location/Qualifiers  
FT rep\_origin 1..654  
FT /tag= a  
FT /note= "ori RK2"  
FT 655..1263  
FT rep\_origin  
FT /tag= b  
FT /note= "ori ColE1"  
FT 1264..2603  
FT /tag= c  
FT /note= "NPT III gene coding for neomycin  
FT phosphotransferase and kanamycin resistance"  
FT 2604..4098  
FT CDS  
FT /tag= d  
FT /note= "TrfA locus from RK2 coding for two proteins P285  
FT and P382 enabling an increase in the replication rate"  
FT 4106..4271  
FT /tag= e  
FT /note= "T-DNA left border"  
FT 4272..4559  
FT /tag= f  
FT /note= "nopaline synthetase terminator"  
FT 4612..5047  
FT /tag= g  
FT /note= "wheat high molecular weight glutenin promoter"  
FT 5096..5627  
FT /tag= h  
FT /note= "rice actin intron"  
FT 5628..7436  
FT /tag= i  
FT /note= "GUS gene coding for beta glucuronidase"  
FT 7437..7763  
FT /tag= j  
FT /note= "nopaline synthetase terminator"  
FT 7763..7936  
FT /tag= k  
FT /note= "T-DNA right border"  
XX  
PN FR2798139-A1.  
XX  
XX  
PD 09-MAR-2001.  
XX  
PF 03-SEP-1999; 99FR-00011112.  
XX  
XX 03-SEP-1999; 99FR-00011112.  
XX  
XX (MERI-) MERISTEM THERAPEUTICS SA.  
XX  
XX Gruber V, Comeau D;  
XX WPI; 2001-259847/27.  
XX  
XX New vector free from non-essential elements, useful for transforming  
PT cells for protein production and for preparing transgenic plants.  
XX  
XX Claim 20; Page 137-140; 180pp; French.  
XX  
XX The specification describes a synthetic vector containing only those  
CC elements essential for its functionality and transgenesis of a cell  
CC (especially a plant cell). The vector consists of at most one origin of  
CC replication (ori), at most one sequence encoding a selection agent and a  
CC trfA locus encoding a protein that increases the level of plasmid  
CC replication. The vector particularly contains an RK2 ori, especially oriV  
CC from pRK2 of Escherichia coli with a broad host range, an antibiotic  
CC resistance gene (especially nptII conferring resistance to kanamycin in  
CC bacteria) and a trfA locus from PRK2 encoding the proteins P285 and P382.

CC The vectors are used to prepare transgenic plants and transformed host  
CC cells for production of a heterologous proteins, e.g. insulin,  
CC interferon, lipase, blood proteins and anti-inflammatory agents. The  
CC present sequence represents a plasmid of the invention  
XX  
SQ

Sequence 7943 BP; 2006 A; 1955 C; 2139 G; 1843 T; 0 U; 0 Other;

Query Match 95.5%; Score 4590.8; DB 4; Length 7943;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 4592; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy	1	CCGGGCTGGTGGCCCTCGCGCTGGGCTGGGCTGGGCGGCGCTGATGGCCCTGCAAAACGCGCCAG	60
Db	1	CCGGGCTGGTGGCCCTCGCGCTGGGCTGGGCGGCGCTGATGGCCCTGCAAAACGCGCCAG	60
Qy	61	AAACGCGCTCGAAGCGCTGTCGAGACACCGCGCGCGCGCTGTCGAGTACCTCGCGG	120
Db	61	AAACGCGCTCGAAGCGCTGTCGAGACACCGCGCGCGCGCTGTCGAGTACCTCGCGG	120
Qy	121	AAACCTTGGCCCTCACTGACAGATGAGGGCGGACGTTGACACTTGAAGGGCGGCACTCAC	180
Db	121	AAACCTTGGCCCTCACTGACAGATGAGGGCGGACGTTGACACTTGAAGGGCGGCACTCAC	180
Qy	181	CCGGCGGCGGCTTGACAGATGAGGGCGAGGCTCGATTTTCGGCGGCGACCTGAGCTGGC	240
Db	181	CCGGCGGCGGCTTGACAGATGAGGGCGAGGCTCGATTTTCGGCGGCGACCTGAGCTGGC	240
Qy	241	CAGCTCGCAATCGGCGAAGCGCTGATTTACGGAGTTCACGGGCGGCACTACTGACAGAT	300
Db	241	CAGCTCGCAATCGGCGAAGCGCTGATTTACGGAGTTCACGGGCGGCACTACTGACAGAT	300
Qy	301	CAAGCTTGGGGAATGAGCTCGGCTGATTTGACACTTGAAGGGCGGCACTACTGACAGAT	360
Db	301	CAAGCTTGGGGAATGAGCTCGGCTGATTTGACACTTGAAGGGCGGCACTACTGACAGAT	360
Qy	361	GAGGGCGGCTTGTGACACTTGAAGGGCGAGTGTGACAGATGAGGGCGGCACTACT	420
Db	361	GAGGGCGGCTTGTGACACTTGAAGGGCGAGTGTGACAGATGAGGGCGGCACTACT	420
Qy	421	TGACATTTGAGGGCTGTGCACAGGCAAGAAATCCAGCAATTTGCAAGGGTTTCGGCCGT	480
Db	421	TGACATTTGAGGGCTGTGCACAGGCAAGAAATCCAGCAATTTGCAAGGGTTTCGGCCGT	480
Qy	481	TTTTTCCGCCACCGCTAACCTGTCTTTTAACTGCTTTTAAACCAATATTTATAAACCCTG	540
Db	481	TTTTTCCGCCACCGCTAACCTGTCTTTTAACTGCTTTTAAACCAATATTTATAAACCCTG	540
Qy	541	TTTTTAAACAGGGCTGCGCCCTGTGCGCGTGACCGCGCACCGGAGGGGGTGCCCCC	600
Db	541	TTTTTAAACAGGGCTGCGCCCTGTGCGCGTGACCGCGCACCGGAGGGGGTGCCCCC	600
Qy	601	CTTCTCGAACCTCCGGAAGGTATGCGGTGTGAATACCGCACAGATCGTAAAGAGA	660
Db	601	CTTCTCGAACCTCCGGAAGGTATGCGGTGTGAATACCGCACAGATCGTAAAGAGA	660
Qy	661	AAATACCGCATCAGGGCTCTTCGGCTTCTCGCTCACTGACTCGCTCGCTCGGCTCGT	720
Db	661	AAATACCGCATCAGGGCTCTTCGGCTTCTCGCTCACTGACTCGCTCGCTCGGCTCGT	720
Qy	721	CGGCTCGGCGAGCGGTATCAGCTCACTCAAGGGCGGTAAATACCGGTATTCACAGAAATCA	780
Db	721	CGGCTCGGCGAGCGGTATCAGCTCACTCAAGGGCGGTAAATACCGGTATTCACAGAAATCA	780
Qy	781	GGGGATAACCGGAAGAAATCATGTGAGCAAAAGGGCGCAAAAGGGCGGAAACCGTAAA	840
Db	781	GGGGATAACCGGAAGAAATCATGTGAGCAAAAGGGCGCAAAAGGGCGGAAACCGTAAA	840
Qy	841	AAGCGCGCTGTGCTGGGCTTTTCCATAGGCTCCGCCCCCTGACGAGCATCAAAAAT	900
Db	841	AAGCGCGCTGTGCTGGGCTTTTCCATAGGCTCCGCCCCCTGACGAGCATCAAAAAT	900
Qy	901	CGACGCTCAAGTCAGAGGTGGGAAACCCGACAGGACTATAAAGATACCAAGCGGTTTCCC	960
Db			

Db	901	CGACGCTCAAGTCAGAGGTGGGAAACCCGACAGGACTATAAAGATACCAAGCGGTTTCCC	960
Qy	961	CTTGGAAAGCTCCCTCGTGGCTCTCTCTGTTCCGACCTCGCTGTTACCGATACCTGCTCC	1020
Db	961	CTTGGAAAGCTCCCTCGTGGCTCTCTCTGTTCCGACCTCGCTGTTACCGATACCTGCTCC	1020
Qy	1021	GCCTTTCTCCCTTCGGGAAAGCGTGGCGCTTTCTCATAGCTCAGCTGTAGGTATCTCAGT	1080
Db	1021	GCCTTTCTCCCTTCGGGAAAGCGTGGCGCTTTCTCATAGCTCAGCTGTAGGTATCTCAGT	1080
Qy	1081	TCGGTGTAGGTGCTTTCGCTCCAAAGCTGGGCTGTGTCAGCAACCCCGCTTCAGCCGAC	1140
Db	1081	TCGGTGTAGGTGCTTTCGCTCCAAAGCTGGGCTGTGTCAGCAACCCCGCTTCAGCCGAC	1140
Qy	1141	CGCTGCGCTTATTCGCTTAACCTATCTGCTTGAAGTCCAAACCGCTTAAGACACGACTTATCG	1200
Db	1141	CGCTGCGCTTATTCGCTTAACCTATCTGCTTGAAGTCCAAACCGCTTAAGACACGACTTATCG	1200
Qy	1201	CCACTGGCAGCAGCTTCTACCATATTCGCGATTAACCCAGCGAAACCAATTTGAGGTGAT	1260
Db	1201	CCACTGGCAGCAGCTTCTACCATATTCGCGATTAACCCAGCGAAACCAATTTGAGGTGAT	1260
Qy	1261	AGGTAAGATTAACCGAGGTATGAAAACGAGAAATGGAACCTTTACAGAAATTAATCTATGA	1320
Db	1261	AGGTAAGATTAACCGAGGTATGAAAACGAGAAATGGAACCTTTACAGAAATTAATCTATGA	1320
Qy	1321	AGCGCCATATTTAAAGCTTACCAAGCAAGAGGATGAAGAGATGAGGAGGAGGAGGATG	1380
Db	1321	AGCGCCATATTTAAAGCTTACCAAGCAAGAGGATGAAGAGATGAGGAGGAGGAGGATG	1380
Qy	1381	CTTGAATATATTGACAACTACTGATAGATAATACATCTTTTATATAGAAAGATATCGCCG	1440
Db	1381	CTTGAATATATTGACAACTACTGATAGATAATACATCTTTTATATAGAAAGATATCGCCG	1440
Qy	1441	TATGTAAGGATTTACGGGGCAAGGATAGGAGCGCGCTTATCAATATATCTATAGAAAT	1500
Db	1441	TATGTAAGGATTTACGGGGCAAGGATAGGAGCGCGCTTATCAATATATCTATAGAAAT	1500
Qy	1501	GGCAAGGATATAAACTTGCATGGAATAATGCTTGAACCCAGGACAAATACCTATAG	1560
Db	1501	GGCAAGGATATAAACTTGCATGGAATAATGCTTGAACCCAGGACAAATACCTATAG	1560
Qy	1561	CTTGTAAATTTACCAAAATTTGGTTCCTCAAAATTCGGCTCGCTGATATCTATAG	1620
Db	1561	CTTGTAAATTTACCAAAATTTGGTTCCTCAAAATTCGGCTCGCTGATATCTATAG	1620
Qy	1621	CMACCTTTGAAAACAACTTTGAAAAGCTGTTTCTGCTGATTTAAAGGTTTGAAGTCAAA	1680
Db	1621	CMACCTTTGAAAACAACTTTGAAAAGCTGTTTCTGCTGATTTAAAGGTTTGAAGTCAAA	1680
Qy	1681	GGAAACAGTGAATTTGGAGTTTCGCTTGTATTAATTTAGCTTCTTGGGGTATCTTTAAATAC	1740
Db	1681	GGAAACAGTGAATTTGGAGTTTCGCTTGTATTAATTTAGCTTCTTGGGGTATCTTTAAATAC	1740
Qy	1741	GTAGAAAAGAGGAAAGGAAATTAATGCTTAAATGAGAAATACCCGGAATTTGAAAAA	1800
Db	1741	GTAGAAAAGAGGAAAGGAAATTAATGCTTAAATGAGAAATACCCGGAATTTGAAAAA	1800
Qy	1801	ACTGATCGAAAATAATACCGCTGCGTAAAGATACGGAAGGAAATGCTCTCTGCTAAGGTATA	1860
Db	1801	ACTGATCGAAAATAATACCGCTGCGTAAAGATACGGAAGGAAATGCTCTCTGCTAAGGTATA	1860
Qy	1861	TGAGCTGGTGGGAAAGTGAACCTATATTTAAATGACGACAGCGGCTATAAAGG	1920
Db	1861	TGAGCTGGTGGGAAAGTGAACCTATATTTAAATGACGACAGCGGCTATAAAGG	1920
Qy	1921	GACCACTATGATGTGGAACCGGAAAGGACATGATGCTATGCTTGGAAAGGAAAGCTGCC	1980
Db	1921	GACCACTATGATGTGGAACCGGAAAGGACATGATGCTATGCTTGGAAAGGAAAGCTGCC	1980
Qy	1981	TGTTCAAAGGCTCTGCACTTTTGAACCGGATGATGCTCGAGCAATCTGCTCATAGTGA	2040
Db	1981	TGTTCAAAGGCTCTGCACTTTTGAACCGGATGATGCTCGAGCAATCTGCTCATAGTGA	2040



Qy	2041	GGCGATGGCGTCTCTTTGCTCGGAGAGTATGAAGATGAACAAGCCCTGAAAGATTAT	2100
Db	2041	GGCGATGGCGTCTCTTTGCTCGGAGAGTATGAAGATGAACAAGCCCTGAAAGATTAT	2100
Qy	2101	CGAGCTGTATGCGGAGTGCATCAGGCTCTTTCACTCCATCGACATATCGGATTGTCCCTA	2160
Db	2101	CGAGCTGTATGCGGAGTGCATCAGGCTCTTTCACTCCATCGACATATCGGATTGTCCCTA	2160
Qy	2161	TACGAATAGCTTACAGACGCGCTTAGCCGAATTGGATTACTTAACGAATACGATCTGGC	2220
Db	2161	TACGAATAGCTTACAGACGCGCTTAGCCGAATTGGATTACTTAACGAATACGATCTGGC	2220
Qy	2221	CGATGGGATGCGAAATCGGGAAGAACCTTGTCTTTTCCACGCGACCTGGG	2280
Db	2221	CGATGGGATGCGAAATCGGGAAGAACCTTGTCTTTTCCACGCGACCTGGG	2280
Qy	2281	TGATTTTTTAAAGACGGAAAGCCGGAAGGAACTTGTCTTTTCCACGCGACCTGGG	2340
Db	2281	TGATTTTTTAAAGACGGAAAGCCGGAAGGAACTTGTCTTTTCCACGCGACCTGGG	2340
Qy	2341	AGACAGCAACATCTTTGTGAAAGATGGCAAAGTAAAGTGGCTTTATTGATCTTGGGAAG	2400
Db	2341	AGACAGCAACATCTTTGTGAAAGATGGCAAAGTAAAGTGGCTTTATTGATCTTGGGAAG	2400
Qy	2401	CGGAGGCGGCAACAGTGGTATGACATTCCTTCGCTCGGTCGATCAGGAGGATAT	2460
Db	2401	CGGAGGCGGCAACAGTGGTATGACATTCCTTCGCTCGGTCGATCAGGAGGATAT	2460
Qy	2461	CGGGGAAGAACAGTATCTCGAGCTATTTTTTGTACTTACCTGGGATCAAGCTGATCGGA	2520
Db	2461	CGGGGAAGAACAGTATCTCGAGCTATTTTTTGTACTTACCTGGGATCAAGCTGATCGGA	2520
Qy	2521	GAAATAAAAATTTATTTACTGGATGAATTTGTTTAGTACTAGATGTCGCGCAACG	2580
Db	2521	GAAATAAAAATTTATTTACTGGATGAATTTGTTTAGTACTAGATGTCGCGCAACG	2580
Qy	2581	ATGCCGCGCAACAGCAGGCGGCAACGACTCTTCCGATCAAGTGTTTGGCTCTCAGG	2640
Db	2581	ATGCCGCGCAACAGCAGGCGGCAACGACTCTTCCGATCAAGTGTTTGGCTCTCAGG	2640
Qy	2641	CCGAGGCGCAAGTATTTGGGCAAGGGTTCGCTGATTCGTCGAGGGCAAGATTC	2700
Db	2641	CCGAGGCGCAAGTATTTGGGCAAGGGTTCGCTGATTCGTCGAGGGCAAGATTC	2700
Qy	2701	GGAAATACCAAGTACGAGAAGGACGGCCAGACGGTCTACGGGACCGACTTCATTGCCGATA	2760
Db	2701	GGAAATACCAAGTACGAGAAGGACGGCCAGACGGTCTACGGGACCGACTTCATTGCCGATA	2760
Qy	2761	AGTGGATTATCTGGACACCAAGGACACGAGCGGTCAAAATCAGGAATAGGGCACATTG	2820
Db	2761	AGTGGATTATCTGGACACCAAGGACACGAGCGGTCAAAATCAGGAATAGGGCACATTG	2820
Qy	2821	CCCCGGGTGAGTCCGGGCAATCCCGCAAGGAGGTGAATCAATCGGACGTTTCACCGGA	2880
Db	2821	CCCCGGGTGAGTCCGGGCAATCCCGCAAGGAGGTGAATCAATCGGACGTTTCACCGGA	2880
Qy	2881	AGGCATACAGGCAAGAACTGATCGACGCGGGTTTTCCGCCGAGGATGCCGAAACCATCG	2940
Db	2881	AGGCATACAGGCAAGAACTGATCGACGCGGGTTTTCCGCCGAGGATGCCGAAACCATCG	2940
Qy	2941	CAAGCCGACCGTATCGGTGCGCCCGCAAACTTCCAGTCCGTCCGATCGGTCC	3000
Db	2941	CAAGCCGACCGTATCGGTGCGCCCGCAAACTTCCAGTCCGTCCGATCGGTCC	3000
Qy	3001	AGCAAGCTACGGCCAAAGATCGAGCGGACGCTGCAACTGGCTCCCCCTGCCCTGCCG	3060
Db	3001	AGCAAGCTACGGCCAAAGATCGAGCGGACGCTGCAACTGGCTCCCCCTGCCCTGCCG	3060
Qy	3061	CGCCATCGGCGCGGTGGAGCGTTTCGCGTCTCTCGAAACAGGAGCGGAGTTTGCGGA	3120
Db	3061	CGCCATCGGCGCGGTGGAGCGTTTCGCGTCTCTCGAAACAGGAGCGGAGTTTGCGGA	3120

Qy	3121	AGTCGATGACCATCGACGCGAGGAACTATGACGACCAAGAGCGAAACCCCGCGG	3180
Db	3121	AGTCGATGACCATCGACGCGAGGAACTATGACGACCAAGAGCGAAACCCCGCGG	3180
Qy	3181	AGGACCTGGCAAAACAGGTACGAGGCGCAAGCAGGCGCGGTTGCTGAAACACACGAAGC	3240
Db	3181	AGGACCTGGCAAAACAGGTACGAGGCGCAAGCAGGCGCGGTTGCTGAAACACACGAAGC	3240
Qy	3241	AGCAGATCAAGGAAATGCGACTTTCCTTGTTCGATATTCGCGCTGCGGACACGATGC	3300
Db	3241	AGCAGATCAAGGAAATGCGACTTTCCTTGTTCGATATTCGCGCTGCGGACACGATGC	3300
Qy	3301	GAGCGATGCCAAACGACACGCGCGCTCTGCTTTCACCAACGCGCAACAAAGAAATCC	3360
Db	3301	GAGCGATGCCAAACGACACGCGCGCTCTGCTTTCACCAACGCGCGCAACAAAGAAATCC	3360
Qy	3361	CGCGGAGGCGCTGCAAAACAAAGTCAATTTTCACTCAACAAAGGACGTGAAGATCACCT	3420
Db	3361	CGCGGAGGCGCTGCAAAACAAAGTCAATTTTCCACGTCAACAAAGGACGTGAAGATCACCT	3420
Qy	3421	ACACCGGCTCGAGCTGCGGGCGGATGACGAACTGGTGTGGCAGCAGGTCTTGGAGT	3480
Db	3421	ACACCGGCTCGAGCTGCGGGCGGATGACGAACTGGTGTGGCAGCAGGTCTTGGAGT	3480
Qy	3481	ACCGGAGCGCACCCCTATCGCGAGCGGATCACTTTCACGTTCTACGAGCTTTGCCAGG	3540
Db	3481	ACCGGAGCGCACCCCTATCGCGAGCGGATCACTTTCACGTTCTACGAGCTTTGCCAGG	3540
Qy	3541	ACCTGGCTGGTTCGATCAATTCGCGGCTTTTACGAAAGCGCGAGGAATGCTGTGCGGCC	3600
Db	3541	ACCTGGCTGGTTCGATCAATTCGCGGCTTTTACGAAAGCGCGAGGAATGCTGTGCGGCC	3600
Qy	3601	TACAGGCGAGCGGATGGGCTTCACTCCGACCGCTGGGACCTTGGAACTCGGTGTCG	3660
Db	3601	TACAGGCGAGCGGATGGGCTTCACTCCGACCGCTGGGACCTTGGAACTCGGTGTCG	3660
Qy	3661	TGCTGCAACCGCTTCCGCGTCTCGGACCGTGGCAAGAAACGTCCTGTCGAGGCTCTGA	3720
Db	3661	TGCTGCAACCGCTTCCGCGTCTCGGACCGTGGCAAGAAACGTCCTGTCGAGGCTCTGA	3720
Qy	3721	TCGACGAGGAAATTCGTGCTGTTTGTGGCGACCACTACAGAAATTCATATGGGAGA	3780
Db	3721	TCGACGAGGAAATTCGTGCTGTTTGTGGCGACCACTACAGAAATTCATATGGGAGA	3780
Qy	3781	AGTACCGAGCTGTCCGACGCGCGGATGTTTCGACTATTCAGCTTCGACCCGGG	3840
Db	3781	AGTACCGAGCTGTCCGACGCGCGGATGTTTCGACTATTCAGCTTCGACCCGGG	3840
Qy	3841	AGCGTACCCGCTCAAGCTGGAACCTTCCGCTCATGTGCGGATCGGATTCACCCCGG	3900
Db	3841	AGCGTACCCGCTCAAGCTGGAACCTTCCGCTCATGTGCGGATCGGATTCACCCCGG	3900
Qy	3901	TGAAGAGTCCGCGAGCAGGTTCGGGAGCTTCGGAAGAGTTTCGAGGAGCGGCTTGG	3960
Db	3901	TGAAGAGTCCGCGAGCAGGTTCGGGAGCTTCGGAAGAGTTTCGAGGAGCGGCTTGG	3960
Qy	3961	TGGAACGCGCTGGGTCAATGATGACTGGTGCATTCGAAACGCTAGGGCTTGTGGGT	4020
Db	3961	TGGAACGCGCTGGGTCAATGATGACTGGTGCATTCGAAACGCTAGGGCTTGTGGGT	4020
Qy	4021	CAGTTCGCGTGGGGTTTACGACGCGCTTACTTGGCAATTCCTAGGTTCGACGCTT	4080
Db	4021	CAGTTCGCGTGGGGTTTACGACGCGCTTACTTGGCAATTCCTAGGTTCGACGCTT	4080
Qy	4081	CTGATGGGCTGCCTGTATCGAGTGGTGAATTTGTGCGGAGCTGCGGTTCGGGAGCTGTT	4140
Db	4081	CTGATGGGCTGCCTGTATCGAGTGGTGAATTTGTGCGGAGCTGCGGTTCGGGAGCTGTT	4140
Qy	4141	GGCTGGCTGGCGAGGATATTTGGTGTGAACAAATTCAGCTTTCAGCACTTAATA	4200
Db	4141	GGCTGGCTGGCGAGGATATTTGGTGTGAACAAATTCAGCTTTCAGCACTTAATA	4200
Qy	4201	ACACATTCGCGACGTTTTTAAATGTTAGTGGGCTATCCCCGGGGGATATCCATAGGCCG	4260



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Db 4201 ACACATTGCGGACGTTTTTAAATGTAATCTGGGCTATCCCGGGGATATCCATAGGCCCG 4260
Qy 4261 ATCTAGTAACATAATGACACCGCGCGATAAATTATCTAGTTTGGCGCTATATTTTG 4320
Db 4261 ATCTAGTAACATAATGACACCGCGCGATAAATTATCTAGTTTGGCGCTATATTTTG 4320
Qy 4321 TTTTCTATCGCGTATTAAATGTATAATTGGGGACTCTAATATATAAAACCCATCTCAT 4380
Db 4321 TTTTCTATCGCGTATTAAATGTATAATTGGGGACTCTAATATATAAAACCCATCTCAT 4380
Qy 4381 AATAACGTGATGATACATGTTAATTATTACATGCTTAACGTTAATTCACAGAAATTAT 4440
Db 4381 AATAACGTGATGATACATGTTAATTATTACATGCTTAACGTTAATTCACAGAAATTAT 4440
Qy 4441 ATGATAATCATCGCAACCGCGCAACAGGATTCATCTTAAGAACTTTATTCGCAATG 4500
Db 4441 ATGATAATCATCGCAACCGCGCAACAGGATTCATCTTAAGAACTTTATTCGCAATG 4500
Qy 4501 TTTGAACGATCGTTTCGTCGAGCTATGGCCCGAGCTTGGCCGCCGTTAACACGCGTGG 4560
Db 4501 TTTGAACGATCGTTTCGTCGAGCTATGGCCCGAGCTTGGCCGCCGTTAACACGCGTGG 4560
Qy 4561 ATCCTTAATTAAAGTCGACTCTAGAGAATTCACTC 4594
Db 4561 ATCCTTAATTAAAGTCGACTCTAGAGAATTCAATC 4594

RESULT 3
AAF80295
ID AAF80295 standard; DNA; 10003 BP.
XX
AC AAF80295;
XX
DT 29-JUN-2001 (first entry)
XX
DE Nucleotide sequence of plasmid pMRT1210.
XX
KW Vector; transgenesis; trfA locus; RK2 ori; oriV; P285 protein;
KW P382 protein; antibiotic resistance gene; nptIII; transgenic plant; ss.
XX Synthetic.
OS
XX Key
XX Location/Qualifiers
FH 1. .654
FT /*tag= a
FT /note= "ori RK2"
FT 655. .1263
FT /*tag= b
FT /note= "ori ColEI"
FT 1264. .2603
FT /*tag= c
FT /note= "NPT III gene coding for neomycin
FT phosphotransferase and kanamycin resistance"
FT 2604. .4098
FT /*tag= d
FT /note= "trfA locus from RK2 coding for two proteins P285
FT and P382 enabling an increase in the replication rate"
FT 4106. .4271
FT /*tag= e
FT /note= "T-DNA left border"
FT 4272. .4559
FT /*tag= f
FT /note= "nopaline synthetase terminator"
FT 4594. .5169
FT /*tag= g
FT /note= "Bar gene coding for phosphinotricin
FT acetyltransferase and glufosinate resistance"
FT 5170. .5704
FT /*tag= h
FT /note= "rice actin intron"
FT 5705. .6638
FT /*tag= i
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FT /note= "rice actin promoter"
FT 6672. .7107
FT /*tag= j
FT /note= "wheat high molecular weight glutenin promoter"
FT 7169. .7687
FT /*tag= k
FT /note= "rice actin intron"
FT 7688. .9496
FT /*tag= l
FT /note= "GUS gene coding for beta glucuronidase"
FT 9497. .9823
FT /*tag= m
FT /note= "nopaline synthetase terminator"
FT 9823. .9996
FT /*tag= n
FT /note= "T-DNA right border"
XX
FN FR2798139-AL.
XX
PD 09-MAR-2001.
XX
PF 03-SEP-1999; 99FR-00011112.
XX
PR 03-SEP-1999; 99FR-00011112.
XX
PA (MERI-) MERISTEM THERAPEUTICS SA.
XX
PI Gruber V, Comeau D;
XX
DR WPI; 2001-259847/27.
XX
PT New vector free from non-essential elements, useful for transforming
PT cells for protein production and for preparing transgenic plants.
XX
PS Claim 20; Page 163-166; 180pp; French.
XX
CC The specification describes a synthetic vector containing only those
CC elements essential for its functionality and transgenesis of a cell
CC (especially a plant cell). The vector consists of at most one origin of
CC replication (ori), at most one sequence encoding a selection agent and a
CC trfA locus encoding a protein that increases the level of plasmid
CC replication. The vector particularly contains an RK2 ori, especially oriV
CC from pRK2 of Escherichia coli with a broad host range, an antibiotic
CC resistance gene (especially nptIII conferring resistance to kanamycin in
CC bacteria) and a trfA locus from pRK2 encoding the proteins P285 and P382.
CC The vectors are used to prepare transgenic plants and transformed host
CC cells for production of a heterologous proteins, e.g. insulin,
CC interferon, lipase, blood proteins and anti-inflammatory agents. The
CC present sequence represents a plasmid of the invention
XX
SQ Sequence 10003 BP; 2476 A; 2470 C; 2729 G; 2328 T; 0 U; 0 Other;

Query Match 94.7%; Score 4549; DB 4; Length 10003;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGGGCTGTTGCCCTCGCGCTGGCTGGCGCGCTCTATGCGCTTGCCTGCAACGCGCCAG 60
Db 1 CGGGGCTGTTGCCCTCGCGCTGGCTGGCGCGCTCTATGCGCTTGCCTGCAACGCGCCAG 60
Qy 61 AAACGCGCTGCAAGCCGTGTGCGAGACACCGCGCGCGCGCGCTTGTGGATACCTCGCG 120
Db 61 AAACGCGCTGCAAGCCGTGTGCGAGACACCGCGCGCGCGCTTGTGGATACCTCGCG 120
Qy 121 AAACCTTGGCCCTCACTGACAGATGAGGGCGGACGTTGACACTTGAAGGGCGGACTCAC 180
Db 121 AAACCTTGGCCCTCACTGACAGATGAGGGCGGACGTTGACACTTGAAGGGCGGACTCAC 180
Qy 181 CGGGCGCGGCTTGACAGATGAGGGCGGACGTTGCTGCTTGGCGCGGCGAGTGGAGTGGC 240
Db 181 CGGGCGCGGCTTGACAGATGAGGGCGGACGTTGCTGCTTGGCGCGGCGAGTGGAGTGGC 240
Qy 241 CAGCCTCGCAAAATCGGGCAAAACGCGCTGATTTTACGCGAGTTTCCCAAGATGATGTGGA 300
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QY 2461 CGGGGAAGAACAGTATGTCGAGCTATTTTGTGACTTACTGGGATCAAGCTGATTGGGA 2520
DB |||||
DB 2461 CGGGGAAGAACAGTATGTCGAGCTATTTTGTGACTTACTGGGATCAAGCTGATTGGGA 2520
QY 2521 GAAAAATAAATAATATTTATTTTACTGGATGAATTTGTTTGTAGTACTAGATGCGGCAACG 2580
DB |||||
DB 2521 GAAAAATAAATAATATTTTACTGGATGAATTTGTTTGTAGTACTAGATGCGGCAACG 2580
QY 2581 ATCGCGCGACAGCAGGAGCGACCGACTTCTTCGCGCATCAAGTGTGTTTGGCTCTCAGG 2640
DB |||||
DB 2581 ATCGCGCGACAGCAGGAGCGACCGACTTCTTCGCGCATCAAGTGTGTTTGGCTCTCAGG 2640
QY 2641 CCGAGGCCCAAGCAAGTATTTGGGCAAGGGGTCGCTGGTATTCGTCAGGCGCAAGATTTC 2700
DB |||||
DB 2641 CCGAGGCCCAAGCAAGTATTTGGGCAAGGGGTCGCTGGTATTCGTCAGGCGCAAGATTTC 2700
QY 2701 GGAATACCAAGTACGAGAAAGGACGGCCAGACGGTCTACGGGACCGACTTCATTTCGCGATA 2760
DB |||||
DB 2701 GGAATACCAAGTACGAGAAAGGACGGCCAGACGGTCTACGGGACCGACTTCATTTCGCGATA 2760
QY 2761 AGGTGGATTATCTGGACACCAAGGCACAGGCGGGTCAAAATCAGGAATAAGGGGCAATTG 2820
DB |||||
DB 2761 AGGTGGATTATCTGGACACCAAGGCACAGGCGGGTCAAAATCAGGAATAAGGGGCAATTG 2820
QY 2821 CCCCGCGTCGAGTCGGGGCAATCCCGCAAGGAGGGTGAATGAATCGGACGTTTTCACCGGA 2880
DB |||||
DB 2821 CCCCGCGTCGAGTCGGGGCAATCCCGCAAGGAGGGTGAATGAATCGGACGTTTTCACCGGA 2880
QY 2881 AGGCATACAGGCAAGAACTGATCGACGCGGGTTTTCCGCGGAGGATGCGCAAAACCATCG 2940
DB |||||
DB 2881 AGGCATACAGGCAAGAACTGATCGACGCGGGTTTTCCGCGGAGGATGCGCAAAACCATCG 2940
QY 2941 CAAGCGCACCGTCATCGCTGCGCCCGCGAAGACCTTCCAGTCCGTCGGCTCGATGGTCC 3000
DB |||||
DB 2941 CAAGCGCACCGTCATCGCTGCGCCCGCGAAGACCTTCCAGTCCGTCGGCTCGATGGTCC 3000
QY 3001 AGCAAGCTACGGCCAAAGTACGAGCGGACACGCGTGCAACTGGCTCCCGCTCGCCCTGCGCCG 3060
DB |||||
DB 3001 AGCAAGCTACGGCCAAAGTACGAGCGGACACGCGTGCAACTGGCTCCCGCTCGCCCTGCGCCG 3060
QY 3061 CGGCATCGCGCGCGTGGAGCGTTTCGCTCGTCTCGAAACAGGAGGCGGCAAGTTTGGCGA 3120
DB |||||
DB 3061 CGGCATCGCGCGCGTGGAGCGTTTCGCTCGTCTCGAAACAGGAGGCGGCAAGTTTGGCGA 3120
QY 3121 AGTCGATGACCATCGACACGCGAGGAACATATGACGACCAAGAAAGCGAAACCCCGCGCG 3180
DB |||||
DB 3121 AGTCGATGACCATCGACACGCGAGGAACATATGACGACCAAGAAAGCGAAACCCCGCGCG 3180
QY 3181 AGGACCTGGCAAAACAGGTACGAGGCGCAAGCAGCGCGGTTGCTTGAAACACACGAAGC 3240
DB |||||
DB 3181 AGGACCTGGCAAAACAGGTACGAGGCGCAAGCAGCGCGGTTGCTTGAAACACACGAAGC 3240
QY 3241 AGCAGATCAAGGAAATGCACTTTCTTGTTCGATATTCGCGCGTGGCGGACACGATGC 3300
DB |||||
DB 3241 AGCAGATCAAGGAAATGCACTTTCTTGTTCGATATTCGCGCGTGGCGGACACGATGC 3300
QY 3301 GAGCGATGCCAAACGACACGGCCCGCTTCGCCCTGTTTCCACGCGCGCAACGAATAATCC 3360
DB |||||
DB 3301 GAGCGATGCCAAACGACACGGCCCGCTTCGCCCTGTTTCCACGCGCGCAACGAATAATCC 3360
QY 3361 CCGCGGAGGGCTGCAAAACAAGTCAATTTCCACGTCAACAGGACGTGAAGATCACCT 3420
DB |||||
DB 3361 CCGCGGAGGGCTGCAAAACAAGTCAATTTCCACGTCAACAGGACGTGAAGATCACCT 3420
QY 3421 ACACCGCGTCGAGCTGCGGGCCGACGATGACGAACCTGTTGTCGACGAGGTGTCGAGT 3480
DB |||||
DB 3421 ACACCGCGTCGAGCTGCGGGCCGACGATGACGAACCTGTTGTCGACGAGGTGTCGAGT 3480
QY 3481 ACSGGAAGCGCACCCCTATCGGCGAGCGGATCACTTTCAGGCTTTCAGGAGCTTTGCCAGG 3540
DB |||||
DB 3481 ACSCGAAGCGCACCCCTATCGGCGAGCGGATCACTTTCAGGCTTTCAGGAGCTTTGCCAGG 3540
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QY 3541 ACCTGGCTGGTCGATCAATGGCCGGTATTTACAGGAAGCCGAGGAATGCTGTGCGGCC 3600
DB |||||
DB 3541 ACCTGGCTGGTCGATCAATGGCCGGTATTTACAGGAAGCCGAGGAATGCTGTGCGGCC 3600
QY 3601 TACAGCGACGGCGATGGGCTTCACGTCCGACCGCGTTGGGCACTTGGAAATCGGTGTGCG 3660
DB |||||
DB 3601 TACAGCGACGGCGATGGGCTTCACGTCCGACCGCGTTGGGCACTTGGAAATCGGTGTGCG 3660
QY 3661 TGTCTCACCGCTTCCCGCTCTCGACCGTGGCAAGAAACGTCCTCGTTGCCAGTCTCTGA 3720
DB |||||
DB 3661 TGTCTCACCGCTTCCCGCTCTCGACCGTGGCAAGAAACGTCCTCGTTGCCAGTCTCTGA 3720
QY 3721 TCACAGAGGAAATCGTCGTGCTGTTTGTCTGGCGACCACTACACGAAATTCATATGGGAGA 3780
DB |||||
DB 3721 TCACAGAGGAAATCGTCGTGCTGTTTGTCTGGCGACCACTACACGAAATTCATATGGGAGA 3780
QY 3781 AGTACCGCAAGCTGTCCGACGGCCGCGAGCGATGTTTGCATATTTTCAGCTCGACCGGG 3840
DB |||||
DB 3781 AGTACCGCAAGCTGTCCGACGGCCGCGAGCGATGTTTGCATATTTTCAGCTCGACCGGG 3840
QY 3841 AGCGGTACCGCTCAAGCTGGAAACCTTCCGCTCATGTGCGGATCGGATTCACCCGCG 3900
DB |||||
DB 3841 AGCGGTACCGCTCAAGCTGGAAACCTTCCGCTCATGTGCGGATCGGATTCACCCGCG 3900
QY 3901 TGAAGAAAGTGGCGGACGAGGTGCGGAAAGCCTTCGAAAGATTTGCAGGCGAGCGGCTGG 3960
DB |||||
DB 3901 TGAAGAAAGTGGCGGACGAGGTGCGGAAAGCCTTCGAAAGATTTGCAGGCGAGCGGCTGG 3960
QY 3961 TGAACACCGCTGGGTCAATGATGACCTGGTGCATTTGCAAAACGCTAGGGGCTTTGTGGGGT 4020
DB |||||
DB 3961 TGAACACCGCTGGGTCAATGATGACCTGGTGCATTTGCAAAACGCTAGGGGCTTTGTGGGGT 4020
QY 4021 CAGTTCGGCTGGGGTTTCAGCAGCGAGCGCTTTTACTGCGATTTCTTAGGTTCACGCTTT 4080
DB |||||
DB 4021 CAGTTCGGCTGGGGTTTCAGCAGCGAGCGCTTTTACTGCGATTTCTTAGGTTCACGCTTT 4080
QY 4081 CTGATGGGCTGCTGATCGAGTGGTGAATTTGTGCGAGCTGCCGCTCGGGGAGCTGTT 4140
DB |||||
DB 4081 CTGATGGGCTGCTGATCGAGTGGTGAATTTGTGCGAGCTGCCGCTCGGGGAGCTGTT 4140
QY 4141 GGTGCTGGTGGCGAGGATATATTTGGTGTGAACAAATTTAGCGCTTAGCAACTTAATA 4200
DB |||||
DB 4141 GGTGCTGGTGGCGAGGATATATTTGGTGTGAACAAATTTAGCGCTTAGCAACTTAATA 4200
QY 4201 ACACATTCGGGAGCTTTTAAATGCTACTGGGGCTATCCCGGGGGATATCCCATAGGCCCG 4260
DB |||||
DB 4201 ACACATTCGGGAGCTTTTAAATGCTACTGGGGCTATCCCGGGGGATATCCCATAGGCCCG 4260
QY 4261 ATCTAGTAACATAATGACACCGCGCGGATAATTTATCTTAGTTTCGGCGCTATATTTTG 4320
DB |||||
DB 4261 ATCTAGTAACATAATGACACCGCGCGGATAATTTATCTTAGTTTCGGCGCTATATTTTG 4320
QY 4321 TTTTCTATCGGTAATTAATGATATATTTAGTGGGACTCTAATCATATAAAACCCATCTCAT 4380
DB |||||
DB 4321 TTTTCTATCGGTAATTAATGATATATTTAGTGGGACTCTAATCATATAAAACCCATCTCAT 4380
QY 4381 AATAACGTCATGCAATTCATATTAATTAATGCTTAACGTAATTAACAGAAATTAAT 4440
DB |||||
DB 4381 AATAACGTCATGCAATTCATATTAATTAATGCTTAACGTAATTAACAGAAATTAAT 4440
QY 4441 ATGATTAATCATCGCAAGACCGGCAACAGGATTCATCTTAAGAAACCTTTATTCGCAATG 4500
DB |||||
DB 4441 ATGATTAATCATCGCAAGACCGGCAACAGGATTCATCTTAAGAAACCTTTATTCGCAATG 4500
QY 4501 TTTGAACGATCGTTCGTCAGCTATGGGCCCGAAGCTTGGCGGCCGTT 4549
DB |||||
DB 4501 TTTGAACGATCGTTCGTCAGCTATGGGCCCGAAGCTTGGCGGCCGTT 4549
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RESULT 4  
AAF80290  
ID AAF80290 standard; DNA; 5614 BP.  
XX



Qy	961	CCTCGAAGCTCCGCTCGTGGCGCTCTCTGTTCCGAGCCCTGCCGCTTACCGGATACCTGTGCC	1021
Db	961	CCTGGAAGCTCCCTCGTGGCGCTCTCTGTTCCGAGCCCTGCCGCTTACCGGATACCTGTGCC	1020
Qy	1021	GCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTCTAGGTATCTCAGT	1080
Db	1021	GCCTTTCTCCCTTCGGGNAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGT	1080
Qy	1081	TCGCTGTAGTGTTCGCTCCAAAGCTCGGCTGTGTGCAAGAAACCCCGCTTACGCCCGAC	1140
Db	1081	TCGCTGTAGTGTTCGCTCCAAAGCTCGGCTGTGTGCAAGAAACCCCGCTTACGCCCGAC	1140
Qy	1141	CGCTGGCGCTTATCCGGTAACTATCGTCTTGAGTCTCAACCGGTGAACACAGCACTTATCG	1200
Db	1141	CGCTGGCGCTTATCCGGTAACTATCGTCTTGAGTCTCAACCGGTGAACACAGCACTTATCG	1200
Qy	1201	CCACTGGCAGCAGCTTCTACCAATAATCCGCGATAAACCCAGCGAAACATTTTCAGGTGAT	1260
Db	1201	CCACTGGCAGCAGCTTCTACCAATAATCCGCGATAAACCCAGCGAAACATTTTCAGGTGAT	1260
Qy	1261	AGGTAAAGTATATACCGAGGTATGAAACAGAGAAITTGACCTTTACAGAAITTACTCTATGA	1320
Db	1261	AGGTAAAGTATATACCGAGGTATGAAACAGAGAAITTGACCTTTACAGAAITTACTCTATGA	1320
Qy	1321	AGCCCCATATTTAAAAAGCTTACCAAGACGAGGAGTGAAGAGATGAGGAGGAGCATTG	1380
Db	1321	AGCCCCATATTTAAAAAGCTTACCAAGACGAGGAGTGAAGAGATGAGGAGGAGCATTG	1380
Qy	1381	CTTTGAATATATTGACAAATCTGATAGATAATACATCTTTTATATAGAGATATCGCCG	1440
Db	1381	CTTTGAATATATTGACAAATCTGATAGATAATACATCTTTTATATAGAGATATCGCCG	1440
Qy	1441	TATGTAAGGATTTTCAGGGGGCAAGGCCATAGGCAGCGCTTATCAATATATCTATAGAAT	1500
Db	1441	TATGTAAGGATTTTCAGGGGGCAAGGCATAGGCAGCGCTTATCAATATATCTATAGAAT	1500
Qy	1501	GGGCAAAAGCATAAAACTTGATGGACTAATGCTTGAAACCCAGGACAATAACCTTTATAG	1560
Db	1501	GGGCAAAAGCATAAAACTTGATGGACTAATGCTTGAAACCCAGGACAATAACCTTTATAG	1560
Qy	1561	CTTTGTAATTTCTACCAAAATTTGGTTTTCAAAATCGCTCCGCTCGATCTATGTTATACG	1620
Db	1561	CTTTGTAATTTCTACCAAAATTTGGTTTTCAAAATCGGCTCCGCTCGATCTATGTTATACG	1620
Qy	1621	CCAACCTTTGAAAAACAACCTTTTGAAAAAGCTCTTTTCTGGTATTTTAAAGGTTTAAAGTGC	1680
Db	1621	CCAACCTTTGAAAAACAACCTTTTGAAAAAGCTCTTTTCTGGTATTTTAAAGTGTAAAGTGC	1680
Qy	1681	GGAAACAGTGAATTTGGAGTTTCGTCTTGTTATAATTTAGCTTCTTGGGGTATCTTTTAAAT	1740
Db	1681	GGAAACAGTGAATTTGGAGTTTCGTCTTGTTATAATTTAGCTTCTTGGGGTATCTTTTAAAT	1740
Qy	1741	GTAGAAAAGGAGGAAATAATAATGGCTTAAATGAGNAATATCACCGGAATTGAAAAA	1800
Db	1741	GTAGAAAAGGAGGAAATAATAATGGCTTAAATGAGNAATATCACCGGAATTGAAAAA	1800
Qy	1801	ACTGATCGAAAAATAACCGCTTCGCTTAAAGATAACGGAAGGAAATGCTCTCTGAAGGTATA	1860
Db	1801	ACTGATCGAAAAATAACCGCTTCGCTTAAAGATAACGGAAGGAAATGCTCTCTGAAGGTATA	1860
Qy	1861	TAAAGCTGGTGGGAGAAATGAAAACTTATATTTTAAAAATGACGACACGCCGTATAAAGG	1920
Db	1861	TAAAGCTGGTGGGAGAAATGAAAACTTATATTTTAAAAATGACGACACGCCGTATAAAGG	1920
Qy	1921	GACCACTATGATGTGAAACGGGAAAGGACATGATGCTATGCTGGAAGGAAGCTGCC	1980
Db	1921	GACCACTATGATGTGAAACGGGAAAGGACATGATGCTATGCTGGAAGGAAGCTGCC	1980
Qy	1981	TGTTTCAAAGGTCTCGACCTTTGAAACGGCATGATGCTGGAGCAATCTGCTCATGAGTGA	2040
Db	1981	TGTTTCAAAGGTCTCGACCTTTGAAACGGCATGATGCTGGAGCAATCTGCTCATGAGTGA	2040
Qy	2041	GGCCGATGGCGCTCTTTTGCTCGGAAGAGTATGAAGATGAACAAAGCCCTGAAAAAGATTAT	2100

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Db 3121 AGTCGATGACCGAGGAGGACTATGACGACCAAGAGCAAAACCGCGCG 3180
Qy 3181 AGGACCTGGCAAAACAGGTGAGGAGGCCAAGAGGCGCGGTGCTGTAACACACGAGC 3240
Db 3181 AGGACCTGGCAAAACAGGTGAGGAGGCCAAGAGGCGCGGTGCTGTAACACACGAGC 3240
Qy 3241 AGCAGATCAAGGAAATGCAGCTTTCCTGTTGTCGATATGCGCGTGGCCGACACGATGC 3300
Db 3241 AGCAGATCAAGGAAATGCAGCTTTCCTGTTGTCGATATGCGCGTGGCCGACACGATGC 3300
Qy 3301 GAGCGATGCCAAACGACACGCGCGCTCTGCGCTGTTTCCACGCGCAACAAGAAATCC 3360
Db 3301 GAGCGATGCCAAACGACACGCGCGCTCTGCGCTGTTTCCACGCGCAACAAGAAATCC 3360
Qy 3361 CGCGGAGGCGCTGCAAAAACAAGTCAATTTTCCACGCTCAACAGGAGCGTAAGATCACCT 3420
Db 3361 CGCGGAGGCGCTGCAAAAACAAGTCAATTTTCCACGCTCAACAGGAGCGTAAGATCACCT 3420
Qy 3421 ACACCGCGTCGAGCTCGCGGCGCAGCATGACGAACCTGGTGTGCGCAGCAGGTGTTGAGT 3480
Db 3421 ACACCGCGTCGAGCTCGCGGCGCAGCATGACGAACCTGGTGTGCGCAGCAGGTGTTGAGT 3480
Qy 3481 ACAGGAGCGCACCCCTATCGCGAGCGGATCACCTTTCAGCTTCTACGAGCTTTGCCAGG 3540
Db 3481 ACAGGAGCGCACCCCTATCGCGAGCGGATCACCTTTCAGCTTCTACGAGCTTTGCCAGG 3540
Qy 3541 ACCTGGGCTGGTCGATCAATGGCGGTATTAACGAAAGCGGAGGAATGCTGTGCGGCC 3600
Db 3541 ACCTGGGCTGGTCGATCAATGGCGGTATTAACGAAAGCGGAGGAATGCTGTGCGGCC 3600
Qy 3601 TACAGGCGAGCGGATGGGCTTACGTCGACCGGTTGGGACCTGGAATCGGTGTGCG 3660
Db 3601 TACAGGCGAGCGGATGGGCTTACGTCGACCGGTTGGGACCTGGAATCGGTGTGCG 3660
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Db 3661 TGCTGACCGCTTCCGCGTCTCGACCGTGCAGAGAAAACGTCCTCGTTCAGGCTCCTGA 3720
Qy 3721 TCAGCAGGAAATCGTCTGCTGTTTGTGTCGCGACCACTACACGAAATTCATATGGGAGA 3780
Db 3721 TCAGCAGGAAATCGTCTGCTGTTTGTGTCGCGACCACTACACGAAATTCATATGGGAGA 3780
Qy 3781 AGTACCCCAAGCTTCCGCGAGCGCCGACGGATGTCGATTTTCAGCTCGCACCGGG 3840
Db 3781 AGTACCCCAAGCTTCCGCGAGCGCCGACGGATGTCGATTTTCAGCTCGCACCGGG 3840
Qy 3841 AGCGGTACCCGCTCAAGCTGGAACCTTCCGCTCATGTGCGGATCGGATTTCCACCCGCG 3900
Db 3841 AGCGGTACCCGCTCAAGCTGGAACCTTCCGCTCATGTGCGGATCGGATTTCCACCCGCG 3900
Qy 3901 TGAAGAAGTGGCGGAGCAGGTGCGGAGAGCCTCGGAAGAGTTGCGAGGCGAGCGGCTGG 3960
Db 3901 TGAAGAAGTGGCGGAGCAGGTGCGGAGAGCCTCGGAAGAGTTGCGAGGCGAGCGGCTGG 3960
Qy 3961 TGGACACGCTGGGTCAATGATCACTGGTGCATTCGCAACGCTAGGCGCTTGGGGT 4020
Db 3961 TGGACACGCTGGGTCAATGATCACTGGTGCATTCGCAACGCTAGGCGCTTGGGGT 4020
Qy 4021 CAGTTCCGGCTGGGGTTTACGACGCGCTTTTACTGGCATTTTCTAGGTGACGCTT 4080
Db 4021 CAGTTCCGGCTGGGGTTTACGACGCGCTTTTACTGGCATTTTCTAGGTGACGCTT 4080
Qy 4081 CTGATGGGCTGCCTGTATTCGAGTGGTATTTGTGCCAGTGCCTGCGGGAGCTGTT 4140
Db 4081 CTGATGGGCTGCCTGTATTCGAGTGGTATTTGTGCCAGTGCCTGCGGGAGCTGTT 4140
Qy 4141 GGCTGGCTGGGCGAGGATATATTTGCTGTAAACAAATTCACGCTTAGACAATTAATA 4200
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Qy 4201 ACACATTCGCGACGTTTTTAATGTACTGGGCTATCCCGCGGGGATATCCATAGGCCG 4260
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Db 4321 TTTTCTATCGCGTATTAATATGATATTAATTCGGGAGCTCTAATATATAAAACCCATCTCATA 4380
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Db 4441 ATGATAATCATGCAAGACCGCAACAGGATTCAAATCTTAAGAAAACTTTATTCGCAATG 4500
Qy 4501 TTTGAACGATCGTTCGTCGAGCTATGGGCCGA 4533
Db 4501 TTTGAACGATCGTTCGTCGAGCTATGGGCCGA 4533
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RESULT 5  
AAF80277

ID AAF80277 standard; DNA; 5971 BP.

XX AAF80277;

XX 29-JUN-2001 (first entry)

XX Nucleotide sequence of plasmid pMRT1118.

XX Vector; transgenesis; trfA locus; RK2 ori; oriV; P285 protein;  
KW P382 protein; antibiotic resistance gene; nptIII; transgenic plant; ss.

XX Synthetic.

XX Key Location/Qualifiers

FT rep\_origin 1..654

FT /tag= a

FT /note= "ori RK2"

FT CDS 655..1263

FT /tag= b

FT /note= "NPT III gene coding for neomycin  
phosphotransferase and kanamycin resistance"

FT CDS 2604..4098

FT /tag= c

FT /note= "trfA locus from RK2 coding for two proteins P285  
and P382 enabling an increase in the replication rate"

FT misc\_feature 4106..4271

FT /tag= d

FT /note= "T-DNA left border"

FT terminator 4272..4559

FT /tag= e

FT /note= "nopaline synthetase terminator"

FT CDS 4560..5556

FT /tag= f

FT /note= "NPT III gene coding for neomycin  
phosphotransferase and kanamycin resistance"

FT promoter 5557..5770

FT /tag= g

FT /note= "nopaline synthetase promoter"

FT misc\_feature 5791..5964

FT /tag= h

FT /note= "T-DNA right border"

XX FR2798139-A1.

XX 09-MAR-2001.

XX 03-SEP-1999;

XX 03-SEP-1999;

XX 99FR-00011112.

XX 99FR-00011112.



XX	(MERI-) MERISTEM THERAPEUTICS SA.
PA	Gruber V, Comeau D;
XX	WPI; 2001-259847/27.
XX	New vector free from non-essential elements, useful for transforming cells for protein production and for preparing transgenic plants.
PT	Claim 20; Page 90-92; 180pp; French.
XX	
CC	The specification describes a synthetic vector containing only those elements essential for its functionality and transgenesis of a cell (especially a plant cell). The vector consists of at most one origin of replication (ori), at most one sequence encoding a selection agent and a trfA locus encoding a protein that increases the level of plasmid replication. The vector particularly contains an RK2 ori, especially oriV from pRK2 of Escherichia coli with a broad host range, an antibiotic resistance gene (especially nptII) conferring resistance to kanamycin in bacteria) and a trfA locus from pRK2 encoding the proteins P285 and P382. The vectors are used to prepare transgenic plants and transformed host cells for production of a heterologous proteins, e.g. insulin, interferon, lipase, blood proteins and anti-inflammatory agents. The present sequence represents a plasmid of the invention
XX	
SQ	Sequence 5971 BP; 1501 A; 1513 C; 1657 G; 1300 T; 0 U; 0 Other;
	Query Match 94.3%; Score 4531.4; DB 4; Length 5971;
	Best Local Similarity 100.0%; Pred. No. 0;
	Matches 4532; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY	1 CCGGGCTGGTTCGCCCTGCGCGCTGGGGCTGGCGCGCTCTATGGCCCTGC AAAACGGCCAG 60
DB	1 CCGGGCTGGTTCGCCCTGCGCGCTGGGGCTGGCGCGCTCTATGGCCCTGC AAAACGGCCAG 60
QY	61 AAACGGCGTGAAAGCGGTGTGCGAGACACCGCGCGCGCGGTGTGGATACCTCGCGG 120
DB	61 AAACGGCGTGAAAGCGGTGTGCGAGACACCGCGCGCGCGGTGTGGATACCTCGCGG 120
QY	121 AAAACTTGGCCCTCACTGACAGATGAGGGCGGAGCTTTGACACTTGAGGGGCCACTCAC 180
DB	121 AAAACTTGGCCCTCACTGACAGATGAGGGCGGAGCTTTGACACTTGAGGGGCCACTCAC 180
QY	181 CCGGCGCGCGGTGTGACAGATGAGGGCGAGGCTCGATTTCGGCGCGCGACGTGGAGCTGGC 240
DB	181 CCGGCGCGCGGTGTGACAGATGAGGGCGAGGCTCGATTTCGGCGCGCGACGTGGAGCTGGC 240
QY	241 CAGCCTCGAAATTCGGCGAAAACGGCTGATTTTTACCGAGTTTCCCAGATGATGGGA 300
DB	241 CAGCCTCGAAATTCGGCGAAAACGGCTGATTTTTACCGAGTTTCCCACAGATGATGGGA 300
QY	301 CAAGCTGGGGATAAGTGCCTTCGGGTATTGACACTTGAGGGCGCGACTACTACAGAT 360
DB	301 CAAGCTGGGGATAAGTGCCTTCGGGTATTGACACTTGAGGGCGCGACTACTACAGAT 360
QY	361 GAGGGCGCGATCTTTGACACTTGAGGGCGAGGTGCTGACAGATGAGGGCGCACCTAT 420
DB	361 GAGGGCGCGATCTTTGACACTTGAGGGCGAGGTGCTGACAGATGAGGGCGCACCTAT 420
QY	421 TGACATTTGAGGGGTGTCCACAGCGAGAAAATCCAGCATTTGCAAGGGTTTCGCGCGGT 480
DB	421 TGACATTTGAGGGGTGTCCACAGCGAGAAAATCCAGCATTTGCAAGGGTTTCGCGCGGT 480
QY	481 TTTTCGGCCACCGCTAACCTGTCTTTTAACCTGCTTTTAAACCAATATTTATAAACCTTG 540
DB	481 TTTTCGGCCACCGCTAACCTGTCTTTTAACCTGCTTTTAAACCAATATTTATAAACCTTG 540
QY	541 TTTTAAACAGGGCTGCGCCCTGTGCGGTGACCGCGACCGCGAGGGGGTGC CCCCC 600
DB	541 TTTTAAACAGGGCTGCGCCCTGTGCGGTGACCGCGACCGCGAGGGGGTGC CCCCC 600
QY	601 CTCTCGAAACCCCTCCCGGAAAGGTATGCGGTGTGAAATACCGCACAGATGCGTAAGGAGA 660
DB	601 CTCTCGAAACCCCTCCCGGAAAGGTATGCGGTGTGAAATACCGCACAGATGCGTAAGGAGA 660



Db 1681 GGAAAGTGAATTTGGAGTTCGTCTTGTATTAATAGCTTCTGGGTAATCTTTAAATACT 1740  
Qy 1741 GTAGAAAAGAGGAAGAAATAATAATGGCTAAATAATAGAAATATCACCGGAATGAAAAA 1800  
Db 1741 GTAGAAAAGAGGAAGAAATAATAATGGCTAAATAATAGAAATATCACCGGAATGAAAAA 1800  
Qy 1801 ACTGATCGAAAAATACCGCTGCGTAAAGATACGGAAGGAATCTCTCTGCTAAGGTATA 1860  
Db 1801 ACTGATCGAAAAATACCGCTGCGTAAAGATACGGAAGGAATCTCTCTGCTAAGGTATA 1860  
Qy 1861 TAAGCTGGTGGGAGAAAATGAAAAACCTATATTTAAAAATACAGCAGACCGCGGTATAAAGG 1920  
Db 1861 TAAGCTGGTGGGAGAAAATGAAAAACCTATATTTAAAAATACAGCAGACCGCGGTATAAAGG 1920  
Qy 1921 GACCACCTATGATGTGGAACGGGAAAAAGGACATGATGCTATGCTGGAAGAAAAGCTGCC 1980  
Db 1921 GACCACCTATGATGTGGAACGGGAAAAAGGACATGATGCTATGCTGGAAGAAAAGCTGCC 1980  
Qy 1981 TGTTCMAAGGTCTGCACTTTGAAACGGCATGATGGCTGGAGCAATCTGCTCATGAGTGA 2040  
Db 1981 TGTTCMAAGGTCTGCACTTTGAAACGGCATGATGGCTGGAGCAATCTGCTCATGAGTGA 2040  
Qy 2041 GGCCGATGGCGTCTTTGCTCGGAAGAGTATGAAGTGAACAAAGCCCTGAAAAAGATTAT 2100  
Db 2041 GGCCGATGGCGTCTTTGCTCGGAAGAGTATGAAGTGAACAAAGCCCTGAAAAAGATTAT 2100  
Qy 2101 CGAGCTGTATGCGGAGTGCATAGGCTCTTTCACTCCATCGACATATCGAATTGTCCTTA 2160  
Db 2101 CGAGCTGTATGCGGAGTGCATAGGCTCTTTCACTCCATCGACATATCGAATTGTCCTTA 2160  
Qy 2161 TACGAATAGCTTAGACAGCGCTTAGCCGAATTTGGATTACTTACTGAATAACGATCTGGC 2220  
Db 2161 TACGAATAGCTTAGACAGCGCTTAGCCGAATTTGGATTACTTACTGAATAACGATCTGGC 2220  
Qy 2221 CGATGTGATTTGGAAACCTGGGAAGAACACTTCATTTAAAGATCCGCGCAGCTGTA 2280  
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Qy 2281 TGATTTTTTAAAGACGGAAAGCCCGAAGAGGAATCTGTCTTTTCCACGCGCACTGGG 2340  
Db 2281 TGATTTTTTAAAGACGGAAAGCCCGAAGAGGAATCTGTCTTTTCCACGCGCACTGGG 2340  
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Db 2341 AGACAGCAACATCTTTGTGAAAGATGCAAAAGTAAGTGGCTTTATTTGATCTTGGGAAAG 2400  
Qy 2401 CGGCAGGCGGACAAAGTGGTATGACATTTGCCCTCTGGCTCGGTCGATCAGGGAGGATAT 2460  
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Qy 2461 CGGGGAAGAACAGTATGTCGAGCTATTTTTTGACTTACTTGGGGATCAAGCCTGATGGGA 2520  
Db 2461 CGGGGAAGAACAGTATGTCGAGCTATTTTTTGACTTACTTGGGGATCAAGCCTGATGGGA 2520  
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Db 2521 GAAAAATAAATATATATTTTACTTGGATGAATTTTGTAGTACCTAGATGTCGGCGCAACG 2580  
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Qy 2701 GGAATACCAAGTACAGNAGGACGGCAGACGGTCTACGGACCGCATCTTCAATGCCGATA 2760  
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Db 3901 TGAAGAAGTGGCGGAGCAGGTGGCGAAGCCTGCGAAGAGTTGCGAGGAGCGGCGCTGG 3960  
QY 3961 TGAACAACGCGCTGGGTCAATGATGACCTGTGCTGCAATGCAAACTAGGCGCTTTGGGGT 4020  
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Db 4501 TTTGACGATCGTTCTGCGAGCTATGGGCCCAA 4533

RESULT 6  
ID AAF80280  
AC AAF80280 standard; DNA; 6016 BP.  
XX AAF80280;  
XX  
DT 29-JUN-2001 (first entry)  
XX  
DE Nucleotide sequence of plasmid pMR1122.  
XX  
KW Vector; transgenesis; trfA locus; RK2 ori; oriV; P285 protein;  
KW P382 protein; antibiotic resistance gene; nptIII; transgenic plant; ss.  
XX  
OS Synthetic.

Key Location/Qualifiers  
FH rep\_origin 1..654  
FT /\*tag= a  
FT /note= "ori RK2"  
FT 655..1263  
FT /\*tag= b  
FT rep\_origin  
FT 1264..2603  
FT CDS  
FT /note= "ori ColE1"  
FT /\*tag= c  
FT /note= "NPT III gene coding for neomycin  
FT phosphotransferase and kanamycin resistance"  
FT 2604..4098  
FT /\*tag= d

FT misc\_feature /note= "trfA locus from RK2 coding for two proteins P285  
FT and P382 enabling an increase in the replication rate"  
FT 4106..4271  
FT /\*tag= e  
FT /note= "T-DNA left border"  
FT terminator 4272..4559  
FT /\*tag= f  
FT /note= "Nopaline synthetase terminator"  
FT CDS 4560..5556  
FT /\*tag= g  
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FT phosphotransferase and kanamycin resistance"  
FT promoter 5557..5770  
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FT /note= "T-DNA right border"  
XX  
PN FR2798139-A1.  
XX  
XX 09-MAR-2001.  
XX  
XX 03-SEP-1999; 99FR-00011112.  
XX  
XX 03-SEP-1999; 99FR-00011112.  
XX  
PA (MERI-) MERISTEM THERAPEUTICS SA.  
XX  
XX Gruber V, Comeau D;  
PI  
XX WPI; 2001-259847/27.  
DR  
XX  
XX New vector free from non-essential elements, useful for transforming  
XX cells for protein production and for preparing transgenic plants.  
PT  
XX  
PS Claim 20; Page 101-103; 180pp; French.  
CC  
CC The specification describes a synthetic vector containing only those  
CC elements essential for its functionality and transgenesis of a cell  
CC (especially a plant cell). The vector consists of at most one origin of  
CC replication (ori), at most one sequence encoding a selection agent and a  
CC trfA locus encoding a protein that increases the level of plasmid  
CC replication. The vector particularly contains an RK2 ori, especially oriV  
CC from PRK2 of Escherichia coli with a broad host range, an antibiotic  
CC resistance gene (especially nptIII conferring resistance to kanamycin in  
CC bacteria) and a trfA locus from PRK2 encoding the proteins P285 and P382.  
CC The vectors are used to prepare transgenic plants and transformed host  
CC cells for production of a heterologous proteins, e.g. insulin,  
CC interferon, lipase, blood proteins and anti-inflammatory agents. The  
CC present sequence represents a plasmid of the invention  
XX  
SQ Sequence 6016 BP; 1511 A; 1525 C; 1669 G; 1311 T; 0 U; 0 Other;  
Query Match 94.3%; Score 4531.4; DB 4; Length 6016;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 4532; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 CCGGGCTGTTGCCCTCGCGCTGGCGCTGGCGCGCGCTGATGCGCTGCAAAACGCGCCAG 60  
Db 1 CCGGGCTGTTGCCCTCGCGCTGGCGCTGGCGCGCGCTGATGCGCTGCAAAACGCGCCAG 60  
QY 61 AAACGCGCTCGAAGCGCTGTGCGAGACACCGCGCGCGCGCTTGTGATACCTCGCGG 120  
Db 61 AAACGCGCTCGAAGCGCTGTGCGAGACACCGCGCGCGCGCTTGTGATACCTCGCGG 120  
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QY 181 CCGGGCGCGCTTGACAGATGAGGGCGGAGCTGATTTTCGGCGCGGCGAGCTGAGTGGC 240  
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DB	241	CAGCCTCGCAAAATCGCGGAAACCGCCTGATTTTACGGAGTGTTC	300
QY	301	CAAGCCTGGGGATAAGTGGCCCTCGGTAATTGACACTTGAGGGCGGACTACTGACAGAT	360
DB	301	CAAGCCTGGGGATAAGTGGCCCTCGGTAATTGACACTTGAGGGCGGACTACTGACAGAT	360
QY	361	GAGGGCGCGCATCTTTGACACTTGAGGGCGAGAGTGCTGACAGATGAGGGCGCACCTAT	420
DB	361	GAGGGCGCGCATCTTTGACACTTGAGGGCGAGAGTGCTGACAGATGAGGGCGCACCTAT	420
QY	421	TGACATTTGAGGGGCTGTGCACAGGCGAAGAAATCCAGCATTTTCGAGGGTTCGCGCGGT	480
DB	421	TGACATTTGAGGGGCTGTGCACAGGCGAAGAAATCCAGCATTTTCGAGGGTTCGCGCGGT	480
QY	481	TTTTTCGGCCACCGCTAACCTGTCTTTTAACTCGCTTTTAAACCAATATTTATAAACCTTG	540
DB	481	TTTTTCGGCCACCGCTAACCTGTCTTTTAACTCGCTTTTAAACCAATATTTATAAACCTTG	540
QY	541	TTTTTAAACAGGGCTGCGCCCTGTGCGGTGACCGGCACCGCGAAGGGGGTGCCCCC	600
DB	541	TTTTTAAACAGGGCTGCGCCCTGTGCGGTGACCGGCACCGCGAAGGGGGTGCCCCC	600
QY	601	CTTCTCGAACCCCTCCGCGAAGGTATGCGGTGTGAAATACCGGCACAGATCGTAAGGAGA	660
DB	601	CTTCTCGAACCCCTCCGCGAAGGTATGCGGTGTGAAATACCGGCACAGATCGTAAGGAGA	660
QY	661	AAATACCGCATCAGGCGCTCTCGGCTTCTCGCTCACTGACTCGCTCGGCTCGGTCGTT	720
DB	661	AAATACCGCATCAGGCGCTCTCTCGGCTTCTCGCTCACTGACTCGCTCGGCTCGGTCGTT	720
QY	721	CGGCTGCGGCGAGGGTATCAGCTCACTCAAAGCGGTAAATACGGTTATCCACAGAATCA	780
DB	721	CGGCTGCGGCGAGGGTATCAGCTCACTCAAAGCGGTAAATACGGTTATCCACAGAATCA	780
QY	781	GGGGATAACCGAGAAAGAAATGTGAGCAAAAGGCCAGCAAAAGGCCAGAACCGGTAAA	840
DB	781	GGGGATAACCGAGAAAGAAATGTGAGCAAAAGGCCAGCAAAAGGCCAGAACCGGTAAA	840
QY	841	AAGCCGCGTGTGCGGCTTTTCCATAGGCTCGCCCGCTGACGAGCATCAAAAAAT	900
DB	841	AAGCCGCGTGTGCGGCTTTTCCATAGGCTCGCCCGCTGACGAGCATCAAAAAAT	900
QY	901	CGACGCTCAAGTCAGAGGTGCGAAACCCGACAGGACTATAAGATACCGGCGTTTCCC	960
DB	901	CGACGCTCAAGTCAGAGGTGCGAAACCCGACAGGACTATAAGATACCGGCGTTTCCC	960
QY	961	CTTGGAAAGCTCCCTCGTGGCTCTCCTGTTCCGACCCCTGCGGCTTACCGGATACCTGTCC	1020
DB	961	CTTGGAAAGCTCCCTCGTGGCTCTCCTGTTCCGACCCCTGCGGCTTACCGGATACCTGTCC	1020
QY	1021	GCCTTTCTCCCTTCGGGAAGCGTGGCTTTCTCATAGCTCAGCTGTAGGTATCTCAGT	1080
DB	1021	GCCTTTCTCCCTTCGGGAAGCGTGGCTTTCTCATAGCTCAGCTGTAGGTATCTCAGT	1080
QY	1081	TCGGTGTAGGTGCTTCCGCTCAAGCTGGGCTGTGTGCAAGAACCCCGGTTTACGCCGAC	1140
DB	1081	TCGGTGTAGGTGCTTCCGCTCAAGCTGGGCTGTGTGCAAGAACCCCGGTTTACGCCGAC	1140
QY	1141	CGCTGCGGCTTATCCGGTAACTATCGTCTTGAAGTCCAAACCCGGTAAGACAGCTTATCG	1200
DB	1141	CGCTGCGGCTTATCCGGTAACTATCGTCTTGAAGTCCAAACCCGGTAAGACAGCTTATCG	1200
QY	1201	CCACTGCGAGCGCTTCTACCATAAATCCGCGATAAAACCCAGCAACCATTTGAGGTGAT	1260
DB	1201	CCACTGCGAGCGCTTCTACCATAAATCCGCGATAAAACCCAGCAACCATTTGAGGTGAT	1260
QY	1261	AGGTAAAGATTATCCGAGGTATGAAAACGAGAAATGGACCTTTACAGAAATTTACTATGA	1320
DB	1261	AGGTAAAGATTATCCGAGGTATGAAAACGAGAAATGGACCTTTACAGAAATTTACTATGA	1320

QY	1321	AGCGCCATATTTAAAAAGCTACCAAGACGAAGAGGATGAAGAGGATGAGGAGCGAGATTG	1380
DB	1321	AGCGCCATATTTAAAAAGCTACCAAGACGAAGAGGATGAAGAGGATGAGGAGCGAGATTG	1380
QY	1381	CCTTGAATATATGACAATACTGATAAGATAATACATCTTTTATATAGAAGATATCGCCG	1440
DB	1381	CCTTGAATATATGACAATACTGATAAGATAATACATCTTTTATATAGAAGATATCGCCG	1440
QY	1441	TATGTAAGATTTTACGGGGCAAGGCATAGGCAGCGCTTATCAATATATCTATAGAAT	1500
DB	1441	TATGTAAGATTTTACGGGGCAAGGCATAGGCAGCGCTTATCAATATATCTATAGAAT	1500
QY	1501	GGGCAAGCATAAAACTTGCATGGAATAATGCTTTGAAACCCAGGACAAATACCTTATAG	1560
DB	1501	GGGCAAGCATAAAACTTGCATGGAATAATGCTTTGAAACCCAGGACAAATACCTTATAG	1560
QY	1561	CTTGTAAATTTTACCAAAATTTGGTTTCAAAATCGGCTCCGTGATATCTTAAATACT	1620
DB	1561	CTTGTAAATTTTACCAAAATTTGGTTTCAAAATCGGCTCCGTGATATCTTAAATACT	1620
QY	1621	CCAACTTTGAAACAACTTTGAAAGAGCTTTTCTGGTATTTAAGGTTTGAAGTGA	1680
DB	1621	CCAACTTTGAAACAACTTTGAAAGAGCTTTTCTGGTATTTAAGGTTTGAAGTGA	1680
QY	1681	GGAACTGCAATTTGAGAGTTTCTGTTTAAATTTAGCTTTCTTGGGTTTCTTAAATACT	1740
DB	1681	GGAACTGCAATTTGAGAGTTTCTGTTTAAATTTAGCTTTCTTGGGTTTCTTAAATACT	1740
QY	1741	GTAGAAAAAGAGGAAGAAATAATAATGCTTAAATGAGAAATATCACCGGAATTTGAAAA	1800
DB	1741	GTAGAAAAAGAGGAAGAAATAATAATGCTTAAATGAGAAATATCACCGGAATTTGAAAA	1800
QY	1801	ACTGATCGAAATATACCGCTGCTGTAAGATACGGAAGGAATGCTCTCTGCTAAGGTATA	1860
DB	1801	ACTGATCGAAATATACCGCTGCTGTAAGATACGGAAGGAATGCTCTCTGCTAAGGTATA	1860
QY	1861	TAACTGCTGGGAGAAAAATGAAACCTATATTTAAAAATGACGAGCAGCCGGTATAAAGG	1920
DB	1861	TAACTGCTGGGAGAAAAATGAAACCTATATTTAAAAATGACGAGCAGCCGGTATAAAGG	1920
QY	1921	GACCCTATGATGTGGAACCGGAAAGGACATGATGCTATGGCTGGAAGGAAAGCTGCC	1980
DB	1921	GACCCTATGATGTGGAACCGGAAAGGACATGATGCTATGGCTGGAAGGAAAGCTGCC	1980
QY	1981	TGTTCCAAAGGCTCTGCACTTTTCAAACCGCATGATGCTGGAGCAATCTGCTCATGAGTGA	2040
DB	1981	TGTTCCAAAGGCTCTGCACTTTTCAAACCGCATGATGCTGGAGCAATCTGCTCATGAGTGA	2040
QY	2041	GGCCGATGGGCTCTTTGCTCGGAAGATGAAAGATGAAACAAAGCCCTGAAAAAGATTAT	2100
DB	2041	GGCCGATGGGCTCTTTGCTCGGAAGATGAAAGATGAAACAAAGCCCTGAAAAAGATTAT	2100
QY	2101	CGAGCTGTATGCGGAGTGCATAGGCTCTTTTCACTCCATCGACATATCGGATTTGCCCTA	2160
DB	2101	CGAGCTGTATGCGGAGTGCATAGGCTCTTTTCACTCCATCGACATATCGGATTTGCCCTA	2160
QY	2161	TACGATAGCTTACAGACCGCTTACCGAAATTTGGATTACTTACTGAAATACGATCTGGC	2220
DB	2161	TACGATAGCTTACAGACCGCTTACCGAAATTTGGATTACTTACTGAAATACGATCTGGC	2220
QY	2221	CGATGTGGAATGCGAAAACTTGGGAAGAGACACTCCAATTTAAAGATCCGCGAGCTGTA	2280
DB	2221	CGATGTGGAATGCGAAAACTTGGGAAGAGACACTCCAATTTAAAGATCCGCGAGCTGTA	2280
QY	2281	TGATTTTTTAAAGACGGAAGCCCGAAGAGGAATTGTCTTTTCCACCGGACCTTGGG	2340
DB	2281	TGATTTTTTAAAGACGGAAGCCCGAAGAGGAATTGTCTTTTCCACCGGACCTTGGG	2340
QY	2341	AGACAGCAACATCTTTGTGGAAGATGCAAGTAAAGTGGCTTTATTTGATCTTTGGAGAG	2400
DB	2341	AGACAGCAACATCTTTGTGGAAGATGCAAGTAAAGTGGCTTTATTTGATCTTTGGAGAG	2400
QY	2401	CGGAGGCGGACAAAGTGGTATGACATTTGCTTCTGCTCGGTCGATCAGGGAGGATAT	2460

Db	2401		CGG	CAGGCGG	GAC	AAAGTGG	TATG	AC	ATTGG	CTTCTG	CGTCCG	GTCCG	ATCATC	AGGAGG	A	2460
Qy	2461		CGG	GGAAG	AACAG	TATG	TCTC	GAGCT	ATATTT	TG	ACTT	ACT	TGGG	ATCA	AGCCT	2460
Db	2461		CGG	GGAAG	AACAG	TATG	TCTC	GAGCT	ATATTT	TG	ACTT	ACT	TGGG	ATCA	AGCCT	2460
Qy	2521		G	AAAA	TAAAA	TAT	TAT	TAT	TAT	TAT	TAT	TAT	TAT	TAT	TAT	2580
Db	2521		G	AAAA	TAAAA	TAT	TAT	TAT	TAT	TAT	TAT	TAT	TAT	TAT	TAT	2580
Qy	2581		ATG	CGG	GCG	CAAC	AGG	CGG	CAAC	AGG	CGG	CAAC	AGG	CGG	CAAC	2640
Db	2581		ATG	CGG	GCG	CAAC	AGG	CGG	CAAC	AGG	CGG	CAAC	AGG	CGG	CAAC	2640
Qy	2641		CCG	AGG	CCCA	CGG	CAAG	TAT	TG	GGCA	AGG	CGT	CGT	CGT	CGT	2700
Db	2641		CCG	AGG	CCCA	CGG	CAAG	TAT	TG	GGCA	AGG	CGT	CGT	CGT	CGT	2700
Qy	2701		GGA	ATAC	CAAG	TAT	CGG	AGG	CGG	CAAG	TAT	CGG	AGG	CGG	CAAG	2760
Db	2701		GGA	ATAC	CAAG	TAT	CGG	AGG	CGG	CAAG	TAT	CGG	AGG	CGG	CAAG	2760
Qy	2761		AGT	GG	ATAT	CTG	GAC	CAAC	AGG	CGG	CAAC	AGG	CGG	CAAC	AGG	2820
Db	2761		AGT	GG	ATAT	CTG	GAC	CAAC	AGG	CGG	CAAC	AGG	CGG	CAAC	AGG	2820
Qy	2821		CCC	CGG	CGT	CAG	TCCG	CAAG	GGG	TCA	AGG	CGG	TCA	AGG	CGG	2880
Db	2821		CCC	CGG	CGT	CAG	TCCG	CAAG	GGG	TCA	AGG	CGG	TCA	AGG	CGG	2880
Qy	2881		AGG	CAT	ACAG	CGG	CAAG	TAT	CGG	CGG	CGG	CGG	CGG	CGG	CGG	2940
Db	2881		AGG	CAT	ACAG	CGG	CAAG	TAT	CGG	CGG	CGG	CGG	CGG	CGG	CGG	2940
Qy	2941		CA	AGC	CG	CAAC	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	3000
Db	2941		CA	AGC	CG	CAAC	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	3000
Qy	3001		AG	CAAG	CTAG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	3060
Db	3001		AG	CAAG	CTAG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	3060
Qy	3061		CGC	ATC	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	3120
Db	3061		CGC	ATC	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	3120
Qy	3121		AGT	CG	ATG	CAAC	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	3180
Db	3121		AGT	CG	ATG	CAAC	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	3180
Qy	3181		AGG	AC	TGG	CAAC	AGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	3240
Db	3181		AGG	AC	TGG	CAAC	AGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	3240
Qy	3241		AGC	AG	ATCA	AGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	3300
Db	3241		AGC	AG	ATCA	AGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	3300
Qy	3301		GAG	CG	ATG	CAAC	AGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	3360
Db	3301		GAG	CG	ATG	CAAC	AGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	3360
Qy	3361		CGG	CG	ATG	CAAC	AGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	3420
Db	3361		CGG	CG	ATG	CAAC	AGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	3420
Qy	3421		AC	AC	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	3480
Db	3421		AC	AC	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	3480
Qy	3481		ACG	CG	AGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	3540
Db	3481		ACG	CG	AGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	3540

Db	3481		ACG	CG	AGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	3540
Qy	3541		AC	CTG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	3600
Db	3541		AC	CTG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	3600
Qy	3601		TAC	AGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	3660
Db	3601		TAC	AGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	3660
Qy	3661		TG	CTG	CA	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	3720
Db	3661		TG	CTG	CA	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	3720
Qy	3721		TG	CA	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	3780
Db	3721		TG	CA	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	3780
Qy	3781		AGT	AC	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	3840
Db	3781		AGT	AC	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	3840
Qy	3841		AGC	CGT	AC	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	3900
Db	3841		AGC	CGT	AC	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	3900
Qy	3901		TGA	AG	AGT	GG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	3960
Db	3901		TGA	AG	AGT	GG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	3960
Qy	3961		TG	GA	CA	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	4020
Db	3961		TG	GA	CA	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	4020
Qy	4021		CAG	TT	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	4080
Db	4021		CAG	TT	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	4080
Qy	4081		CTG	AT	GGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	4140
Db	4081		CTG	AT	GGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	4140
Qy	4141		GG	CTG	CT	GG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	4200
Db	4141		GG	CTG	CT	GG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	4200
Qy	4201		AC	CA	TTG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	4260
Db	4201		AC	CA	TTG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	4260
Qy	4261		AT	CT	AGT	CA	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	4320
Db	4261		AT	CT	AGT	CA	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	4320
Qy	4321		TTT	TT	CT	AT	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	4380
Db	4321		TTT	TT	CT	AT	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	4380
Qy	4381		ATA	TA	CGT	CA	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	4440
Db	4381		ATA	TA	CGT	CA	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	4440
Qy	4441		ATG	TA	CGT	CA	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	4500
Db	4441		ATG	TA	CGT	CA	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	4500
Qy	4501		TTT	TA	CGT	CA	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	4533
Db	4501		TTT	TA	CGT	CA	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	CGG	4533

ID AAF80278 standard; DNA; 6016 BP.  
XX AAF80278;  
XX 29-JUN-2001 (first entry)  
XX Nucleotide sequence of plasmid pMRT1119.  
DE Vector; transgenesis; trfA locus; RK2 ori; oriV; P285 protein;  
XX P382 protein; antibiotic resistance gene; nptII; transgenic plant; ss.  
XX Synthetic.  
PH Key Location/Qualifiers  
FT rep\_origin 1..654  
FT /\*tag= a  
FT /note= "ori RK2"  
FT rep\_origin 655..1263  
FT /\*tag= b  
FT /note= "ori ColeI"  
FT CDS 1284..2603  
FT /\*tag= c  
FT /note= "NPT III gene coding for neomycin  
FT phosphotransferase and kanamycin resistance"  
FT CDS 2604..4098  
FT /\*tag= d  
FT /note= "trfA locus from RK2 coding for two proteins P285  
FT and P382 enabling an increase in the replication rate"  
FT misc\_feature 4106..4271  
FT /\*tag= e  
FT /note= "T-DNA left border"  
FT terminator 4272..4559  
FT /\*tag= f  
FT /note= "nopaline synthetase terminator"  
FT CDS 4560..5556  
FT /\*tag= g  
FT /note= "NPT III gene coding for neomycin  
FT phosphotransferase and kanamycin resistance"  
FT promoter 5557..5770  
FT /\*tag= h  
FT /note= "nopaline synthetase promoter"  
FT misc\_feature 5836..6009  
FT /\*tag= i  
FT /note= "T-DNA right border"  
XX FR2798139-A1.  
XX 09-MAR-2001.  
XX 03-SEP-1999; 99FR-00011112.  
XX 03-SEP-1999; 99FR-00011112.  
XX (MERI-) MERISTEM THERAPEUTICS SA.  
XX Gruber V, Comeau D;  
XX WPI; 2001-259847/27.  
XX New vector free from non-essential elements, useful for transforming  
XX cells for protein production and for preparing transgenic plants.  
XX Claim 20; Page 94-96; 180pp; French.  
XX The specification describes a synthetic vector containing only those  
XX elements essential for its functionality and transgenesis of a cell  
XX (especially a plant cell). The vector consists of at most one origin of  
XX replication (ori), at most one sequence encoding a selection agent and a  
XX trfA locus encoding a protein that increases the level of plasmid  
XX replication. The vector particularly contains an RK2 ori, especially oriV  
XX from pRK2 of Escherichia coli with a broad host range, an antibiotic  
XX resistance gene (especially nptII conferring resistance to kanamycin in  
XX bacteria) and a trfA locus from pRK2 encoding the proteins P285 and P382.

CC The vectors are used to prepare transgenic plants and transformed host  
CC cells for production of a heterologous proteins, e.g. insulin,  
CC interferon, lipase, blood proteins and anti-inflammatory agents. The  
CC present sequence represents a plasmid of the invention  
XX  
XX Sequence 6016 BP; 1512 A; 1525 C; 1669 G; 1310 T; 0 U; 0 Other;  
Query Match 94.3%; Score 4531.4; DB 4; Length 6016;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 4532; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 CCGGGCTGGTTGCCCTCGCGCTGGGCTGGCGCCCTCTATGGCCCTGCAAGCGGCCAG 60  
DB 1 CCGGGCTGGTTGCCCTCGCGCTGGGCTGGCGCCCTCTATGGCCCTGCAAGCGGCCAG 60  
QY 61 AAACGGCTGGAAGCGGTGTGCGAGACACCGCGGCCCGCGGTGTGGATACCTCGCGG 120  
DB 61 AAACGGCTGGAAGCGGTGTGCGAGACACCGCGGCCCGCGGTGTGGATACCTCGCGG 120  
QY 121 AAAAATTGGCCCTCACTGACAGATGAGGGCGGACGTTGACACTTGAGGGGCGGACTCAC 180  
DB 121 AAAAATTGGCCCTCACTGACAGATGAGGGCGGACGTTGACACTTGAGGGGCGGACTCAC 180  
QY 181 CCGCGCGCGGTTGACAGATGAGGGCGGACGTTGACACTTGAGGGGCGGACTCAC 240  
DB 181 CCGCGCGCGGTTGACAGATGAGGGCGGACGTTGACACTTGAGGGGCGGACTCAC 240  
QY 241 CAGCCTCGAAATCGGCGAAACGCGCTGATTTACGCGAGTTTCCACACAGATGATGGA 300  
DB 241 CAGCCTCGAAATCGGCGAAACGCGCTGATTTACGCGAGTTTCCACACAGATGATGGA 300  
QY 301 CAAGCTGGGGATAAGTGCCTCGGTATTGACACTTGAGGGGCGGACTTACTGACAGAT 360  
DB 301 CAAGCTGGGGATAAGTGCCTCGGTATTGACACTTGAGGGGCGGACTTACTGACAGAT 360  
QY 361 GAGGGCGCGGATCCTTGACACTTTGAGGGCGAGTGTGACAGATGAGGGGCGGACTTAT 420  
DB 361 GAGGGCGCGGATCCTTGACACTTTGAGGGCGAGTGTGACAGATGAGGGGCGGACTTAT 420  
QY 421 TGACATTTGAGGGGCTGTCCACAGGAGAAATCCAGACTTTCGAGGGTTTCGCGCGT 480  
DB 421 TGACATTTGAGGGGCTGTCCACAGGAGAAATCCAGACTTTCGAGGGTTTCGCGCGT 480  
QY 481 TTTTCGSCACCGCTAACCTGTCTTTTAACTCTTTTAAACCAATATTTATAACCTTG 540  
DB 481 TTTTCGSCACCGCTAACCTGTCTTTTAACTCTTTTAAACCAATATTTATAACCTTG 540  
QY 541 TTTTAAACAGGGCTGCGCCCTGTGCGGTGACCGCGCACCGCGAGGGGGTGCCTCCC 600  
DB 541 TTTTAAACAGGGCTGCGCCCTGTGCGGTGACCGCGCACCGCGAGGGGGTGCCTCCC 600  
QY 601 CTTCTGGAACCTCCCGGAAAGTATGCGGTGTGAATACCGCACAGATCGGTAAAGGA 660  
DB 601 CTTCTGGAACCTCCCGGAAAGTATGCGGTGTGAATACCGCACAGATCGGTAAAGGA 660  
QY 661 AAATACCGCATAGGGCTCTTCGCTTCCTGCTCACTGCTGCTGCTGCTGCTGCTGCT 720  
DB 661 AAATACCGCATAGGGCTCTTCGCTTCCTGCTCACTGCTGCTGCTGCTGCTGCTGCT 720  
QY 721 CCGCTGCGGCGAGCGGTATCAGCTCACTCAAAGCGGTAAATACGTTTATCCAGAAATCA 780  
DB 721 CCGCTGCGGCGAGCGGTATCAGCTCACTCAAAGCGGTAAATACGTTTATCCAGAAATCA 780  
QY 781 GGGGTAACCGAGAAAGACATGTGAGCAAAAGGCGCAGAAAGGCGCAGAAACCGTAAA 840  
DB 781 GGGGTAACCGAGAAAGACATGTGAGCAAAAGGCGCAGAAAGGCGCAGAAACCGTAAA 840  
QY 841 AAGCGCGGTGTGCTGGGGTTTTTCCATAGGCTCGGCCCTTCCAGAGCATCAAAAAT 900  
DB 841 AAGCGCGGTGTGCTGGGGTTTTTCCATAGGCTCGGCCCTTCCAGAGCATCAAAAAT 900  
QY 901 CGACGCTCAAGTCAGAGGTGGCGAAACCGCAGAGGACTATAAGATACAGGGGCTTCCC 960  
DB 901 CGACGCTCAAGTCAGAGGTGGCGAAACCGCAGAGGACTATAAGATACAGGGGCTTCCC 960

Db 901 CGAGCCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAAGGCGTTTCCC 960  
Qy 961 CCTGGAAGCTCCCTCGTCGCTCTCTCTGTTCCGACCCCTGCGCTTACCGGATACCTGTCC 1020  
Db 961 CCTGGAAGCTCCCTCGTCGCTCTCTCTGTTCCGACCCCTGCGCTTACCGGATACCTGTCC 1020  
Qy 1021 GCCTTTCTCCCTTCGGGAAGGTGGCGTTCCTCATAGCTCAGCTCAGCTAGGTACTCAGT 1080  
Db 1021 GCCTTTCTCCCTTCGGGAAGGTGGCGTTCCTCATAGCTCAGCTCAGCTAGGTACTCAGT 1080  
Qy 1081 TCGGTGTAGTTCGCTCCAGCTCGGTGTGTGTCACGAACCCCGCTTCAGCCGAC 1140  
Db 1081 TCGGTGTAGTTCGCTCCAGCTCGGTGTGTGTCACGAACCCCGCTTCAGCCGAC 1140  
Qy 1141 CGCTGCCCTTATCCGGTAACCTATCGTCTTGAAGTCCAAACCCGGTAAGACACGACTTATCG 1200  
Db 1141 CGCTGCCCTTATCCGGTAACCTATCGTCTTGAAGTCCAAACCCGGTAAGACACGACTTATCG 1200  
Qy 1201 CCACTGGCAGAGCTTCTACCAATAATCCGGATAAACCAGCGAAACATTTGAGGTGAT 1260  
Db 1201 CCACTGGCAGAGCTTCTACCAATAATCCGGATAAACCAGCGAAACATTTGAGGTGAT 1260  
Qy 1261 AGGTAAAGTATACCGAGGTATGAAACGAGAAATGCAACCTTTACAGAAATTAATCTATGA 1320  
Db 1261 AGGTAAAGTATACCGAGGTATGAAACGAGAAATGCAACCTTTACAGAAATTAATCTATGA 1320  
Qy 1321 AGGCCATATTTAAAAAGCTACCAAGACGAAGAGATGAAGAGATGAGGAGGCAGATTG 1380  
Db 1321 AGGCCATATTTAAAAAGCTACCAAGACGAAGAGATGAAGAGATGAGGAGGCAGATTG 1380  
Qy 1381 CTTGGAATATATTGACAATACTGATAAGATAAATCAATCTTTTATATAGAAAGATATCGCCG 1440  
Db 1381 CTTGGAATATATTGACAATACTGATAAGATAAATCAATCTTTTATATAGAAAGATATCGCCG 1440  
Qy 1441 TATGTAGGATTTTACGGGGCAGGCAATAGCGAGCGCTTATCAATATATCTATAGAAT 1500  
Db 1441 TATGTAGGATTTTACGGGGCAGGCAATAGCGAGCGCTTATCAATATATCTATAGAAT 1500  
Qy 1501 GGGCAAGCAATAAAACCTTCGATGGACTAATGCTTGAACCCAGGACAATAACCTTATAG 1560  
Db 1501 GGGCAAGCAATAAAACCTTCGATGGACTAATGCTTGAACCCAGGACAATAACCTTATAG 1560  
Qy 1561 CTTGTAAATTTACCAAAATTTGGTTTCAAAATTCGGCTCCGTCGATFACTATGTATACG 1620  
Db 1561 CTTGTAAATTTACCAAAATTTGGTTTCAAAATTCGGCTCCGTCGATFACTATGTATACG 1620  
Qy 1621 CCAACTTTGAAAACAACCTTTGAAAAGCTGTTTTCTGGTATTTAAGGTTTTAGAAATGCAA 1680  
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Db 1681 GGAACAGTGAATTTGGAGTTCTGTTTATAATTTAGCTTCTGGGTATCTTTAAATACT 1740  
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Qy 1861 TAAGCTGGTGGGAGAAATCAAAACCTTATATTTAAAAATGACGACAGCCGGTATAAAG 1920  
Db 1861 TAAGCTGGTGGGAGAAATCAAAACCTTATATTTAAAAATGACGACAGCCGGTATAAAG 1920  
Qy 1921 GACCACCTATGATGTGGAACGGGAAAGGACATGATCTATGCTGGAAGGAAAGCTGCC 1980  
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Qy 2041 GGCCGATGGCGTCTCTTGTCTCGAAGAGTATGAAGATGAACAAAGCCCTGAAAAGATTAT 2100  
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Db 2161 TAGCAATAGCTTAGACAGCGCTTACCGAAATTTGGATTACTTACTGAAATACGATCTGGC 2220  
Qy 2221 CGATGTGGATTTGCGAAAACTGGGAAGAAGACACTCCATTTTAAAGATCCCGCGAGCTGTA 2280  
Db 2221 CGATGTGGATTTGCGAAAACTGGGAAGAAGACACTCCATTTTAAAGATCCCGCGAGCTGTA 2280  
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Qy 2341 AGACAGCAACATCTTTGTGAAAGATGCAAGAGTAAAGTGGCTTTATTGATCTTGGAGAAG 2400  
Db 2341 AGACAGCAACATCTTTGTGAAAGATGCAAGAGTAAAGTGGCTTTATTGATCTTGGAGAAG 2400  
Qy 2401 CGGCAGGGCGGACAAAGTGGTATGACATTCCTCTCGCTCCGTCGATCAGGGAGGATAT 2460  
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Db 2461 CGGGGAAGAACAGTATGTCTGAGCTATTTTGTGCTTACTGGGATCAAGCTGATGGGA 2520  
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Db 2521 GAAAAATAAATAATATATTTTACTGCTGAAATGTTTTAGTACTAGATGTCGGCAACG 2580  
Qy 2581 ATGCCGGCGACAAGCAGAGGACGACCGACTTCTTCGCGCATCAAGTGTTCCTGCTCAGG 2640  
Db 2581 ATGCCGGCGACAAGCAGAGGACGACCGACTTCTTCGCGCATCAAGTGTTCCTGCTCAGG 2640  
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Db 2761 AGGTGATTATCTGGACACCAAGGCACACGAGCGGGTCAAAATCAGGAATTAAGGGCAATTG 2820  
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Db 2941 CAAAGCCGACCGCTATGCGTGGCCCGGAAACCTTTCAGTCCGTCGGCTCGATGGTCC 3000  
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Qy 3061 CGGCATCGCGCGCGTGGAGCGTTGCGTCTGTCGAAACAGGAGCGGCGAGGTTTGGCGA 3120  
Db 3061 CGGCATCGCGCGCGTGGAGCGTTGCGTCTGTCGAAACAGGAGCGGCGAGGTTTGGCGA 3120



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Db |||||
Qy 3181 AGGACCTTGGCAAAACAGGTCAGCGAGGCCAAGCAGCGCGGTTGCTGAAACACACGAGAC 3240
Db |||||
Qy 3181 AGGACCTTGGCAAAACAGGTCAGCGAGGCCAAGCAGCGCGGTTGCTGAAACACACGAGAC 3240
Qy 3241 AGCAGATCAAGGAAATCGACGTTTCCTTGTGTCGATATTTGGCCGCTGCGCCGACACGATGC 3300
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Qy 3241 AGCAGATCAAGGAAATCGACGTTTCCTTGTGTCGATATTTGGCCGCTGCGCCGACACGATGC 3300
Qy 3301 GAGCGATGCCAAAGCAGACGCGCGCTCTGCGCTGTTCCACGCGCAACAGAAATCC 3360
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Qy 3421 ACACGCGCTGAGCTCGCGGCCGACGATGACGAACTGGTGTGCGCAGCAGGTGTGAGT 3480
Db |||||
Qy 3421 ACACGCGCTGAGCTCGCGGCCGACGATGACGAACTGGTGTGCGCAGCAGGTGTGAGT 3480
Qy 3481 ACCGAGACGACCCCTATCGCGAGCGCGATCACCTTCACGTTCTACGAGCTTTGCCAGG 3540
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Qy 3481 ACCGAGACGACCCCTATCGCGAGCGCGATCACCTTCACGTTCTACGAGCTTTGCCAGG 3540
Qy 3541 ACCTGGGCTGGTCATCAATGGCGCGTATTACAGAAAGCGCGAGGAATGCTGTGCGGCC 3600
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Qy 3541 ACCTGGGCTGGTCATCAATGGCGCGTATTACAGAAAGCGCGAGGAATGCTGTGCGGCC 3600
Qy 3601 TACAGGCGAGCGGATGGGTTTCACTGTCGACCGCGTGGGCACCTCGGAATCGGTGTCG 3660
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Qy 3601 TACAGGCGAGCGGATGGGTTTCACTGTCGACCGCGTGGGCACCTCGGAATCGGTGTCG 3660
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Qy 3781 AGTACCGCAAGCTGTGCGCAGCGCCGACGATGTCGATATTTGAGCTCGCAGCGG 3840
Qy 3841 AGCGTACCGCTCAAGCTGGAACCTTCGCGCTCATGTGGGATCGGATTTCCACCGCG 3900
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Qy 3901 TGAAGAAAGTCGCGCAGCAGCTCGCGCAAGCCTCGAAGAGTTGCGAGGCGAGCGCCTGG 3960
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Qy 3901 TGAAGAAAGTCGCGCAGCAGCTCGCGCAAGCCTCGAAGAGTTGCGAGGCGAGCGCCTGG 3960
Qy 3961 TGAACACGCTGGGTCAATGATGACCTGTCGATTTGTCGCGAGCTGCGCGGTGAGCTGTT 4020
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Qy 3961 TGAACACGCTGGGTCAATGATGACCTGTCGATTTGTCGCGAGCTGCGCGGTGAGCTGTT 4020
Qy 4021 CAGTTCGCGCTGGGGTTTCAGCAGCGCGCTTACTGGCAATTTCTAGGTTGACGCTT 4080
Db |||||
Qy 4021 CAGTTCGCGCTGGGGTTTCAGCAGCGCGCTTACTGGCAATTTCTAGGTTGACGCTT 4080
Qy 4081 CTGATGGGCTGCTGTATCGAGTGGTATTTGTCGCGAGCTGCGCGGTGCGGGAGCTGTT 4140
Db |||||
Qy 4081 CTGATGGGCTGCTGTATCGAGTGGTATTTGTCGCGAGCTGCGCGGTGCGGGAGCTGTT 4140
Qy 4141 GGCTGGCTGGTGGCAGGATATATTGTTGTTAAACAAATTCAGCTTAGACAACTTAATA 4200
Db |||||
Qy 4141 GGCTGGCTGGTGGCAGGATATATTGTTGTTAAACAAATTCAGCTTAGACAACTTAATA 4200
Qy 4201 ACACATTCGCGACGTTTTTAATGTACTGGGCTATCCCCGGGGGATATCCATAGGCCG 4260
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Db 4201 ACACATTCGCGACGTTTTTAATGTACTGGGCTATCCCCGGGGATATCCATAGGCCG 4260
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Qy 4261 ATCTAGTAACATATACACCGCGCGGATATTTATCTAGTTTCGGCGCTATATTTG 4320
Qy 4321 TTTTCTATCGGTAATTAATGTATAATTCGGGACTCTAATCAATAAAACCCATCTCAT 4380
Db |||||
Qy 4321 TTTTCTATCGGTAATTAATGTATAATTCGGGACTCTAATCAATAAAACCCATCTCAT 4380
Qy 4381 AATAACGTCATGCAATTCATGTTTAAATTTATTTACATGCTTAAACGTAATTCACAGAAAT 4440
Db |||||
Qy 4381 AATAACGTCATGCAATTCATGTTTAAATTTATTTACATGCTTAAACGTAATTCACAGAAAT 4440
Qy 4441 ATGATTAATTCGCAAGACCGGCAACAGGATTCATCTTAAGAACTTTATTCGCAATG 4500
Db |||||
Qy 4441 ATGATTAATTCGCAAGACCGGCAACAGGATTCATCTTAAGAACTTTATTCGCAATG 4500
Qy 4501 TTTGAACGATCGTTCGTCGAGCTATGGGCCGA 4533
Db |||||
Qy 4501 TTTGAACGATCGTTCGTCGAGCTATGGGCCGA 4533
Db |||||

RESULT 8
AAF80281
ID AAF80281 standard; DNA; 6017 BP.
XX
AC AC
XX AC
DT 29-JUN-2001 (first entry)
XX
DE Nucleotide sequence of plasmid pMRT1155.
XX
KW Vector; transgenesis; trfA locus; RK2 ori; oriV; P285 protein;
P382 protein; antibiotic resistance gene; nprIII; transgenic plant; ss.
XX
OS Synthetic.
FH Key
FT rep_origin 1. .654 Location/Qualifiers
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FT /note= "ori RK2"
FT 655. .1263
FT rep_origin
FT /tag= b
FT /note= "ori Cole1"
FT 1264. .2603
FT CDS
FT /tag= c
FT /note= "NPT III gene coding for neomycin
phosphotransferase and kanamycin resistance"
FT 2604. .4098
FT CDS
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FT /note= "NPT III gene coding for two proteins P285
and P382 enabling an increase in the replication rate"
FT 4106. .4271
FT misc_feature
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FT /note= "T-DNA left border"
FT 4272. .4559
FT terminator
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FT /note= "nopaline synthetase terminator"
FT 4560. .5556
FT CDS
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FT /note= "NPT III gene coding for neomycin
phosphotransferase and kanamycin resistance"
FT 5557. .5771
FT promoter
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FT /note= "nopaline synthetase promoter"
FT 5837. .6010
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XX
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PD	09-MAR-2001.	QY	TTTTTAACGAGGCTCGCCCTGTGCGCGTACCGCGCACCGCGAAGGGGGTGCCTCCC	600
XX		DB		
PF	03-SEP-1999; 99PR-00011112.	DB	TTTTTAACGAGGCTCGCCCTGTGCGCGTACCGCGCACCGCGAAGGGGGTGCCTCCC	600
XX				
PR	03-SEP-1999; 99PR-00011112.	QY	CTTCTCGAACCCCTCCCGGAAAGGTATGCGGTGTGAATACCGCACAGATCGCGTAAGAGA	660
XX		DB		
PA	(MERI-) MERISTEM THERAPEUTICS SA.	DB	CTTCTCGAACCCCTCCCGGAAAGGTATGCGGTGTGAATACCGCACAGATCGCGTAAGAGA	660
XX				
P1	Gruber V, Comeau D;	QY	AAATACCGCATCAGGCGCTCTTCCGCTTCTCGCTCACTCGCTCGCTCGCTCGCTCGCT	720
XX		DB		
DR	WPI; 2001-259847/27.	DB	AAATACCGCATCAGGCGCTCTTCCGCTTCTCGCTCACTCGCTCGCTCGCTCGCTCGCT	720
XX				
PT	New vector free from non-essential elements, useful for transforming	QY	CGCTCGCGAGCGGTATCAGCTCACTCAAGGCGGTAAATACGGTTATCCACAGATCA	780
XX	cells for protein production and for preparing transgenic plants.	DB		
PS	Claim 20; Page 104-106; 180pp; French.	DB	CGCTCGCGAGCGGTATCAGCTCACTCAAGGCGGTAAATACGGTTATCCACAGATCA	780
XX		QY	GGGGATAACGACGAGAAAGAACATGTGAGCAAAAGGCGAGCAAAAGGCGAGGAAACCTGAA	840
CC	The specification describes a synthetic vector containing only those	DB		
CC	elements essential for its functionality and transgenesis of a cell	DB	GGGGATAACGACGAGAAAGAACATGTGAGCAAAAGGCGAGCAAAAGGCGAGGAAACCTGAA	840
CC	(especially a plant cell). The vector consists of at most one origin of	QY	AAAGCGCGCTTGTGCGCTTTTCCATAGCTCCGCGCCCTCGACGAGCATCAAAAT	900
CC	replication (ori), at most one sequence encoding a selection agent and a	DB		
CC	trfA locus encoding a protein that increases the level of plasmid	DB	AAGCGCGCTTGTGCGCTTTTCCATAGCTCCGCGCCCTCGACGAGCATCAAAAT	900
CC	replication. The vector particularly contains an RK2 ori, especially oriv	DB		
CC	from PRK2 of Escherichia coli with a broad host range, an antibiotic	QY	CGACGCTCAAGTCAGAGGTGGGAAACCCGACAGACTATAAAGATACACGAGGCTTTCC	960
CC	resistance gene (especially nptII conferring resistance to kanamycin in	DB		
CC	bacteria) and a trfA locus from PRK2 encoding the proteins P285 and P382.	DB	CGACGCTCAAGTCAGAGGTGGGAAACCCGACAGACTATAAAGATACACGAGGCTTTCC	960
CC	The vectors are used to prepare transgenic plants and transformed host	QY	CTTGAAGCTCCCTCGTGGCTCTCTGTTTCGACCTCGCGCTTACCGGATACCTGTTC	1020
CC	cells for production of a heterologous proteins, e.g. insulin,	DB		
CC	interferon, lipase, blood proteins and anti-inflammatory agents. The	DB	CTTGAAGCTCCCTCGTGGCTCTCTGTTTCGACCTCGCGCTTACCGGATACCTGTTC	1020
CC	present sequence represents a plasmid of the invention	QY	GCCTTTCTCCCTTCGGGAAGCGTGGCGCTTCTCATAGCTCAGCTGTAGGTATCTCAGT	1080
XX		DB		
SQ	Sequence 6017 BP; 1512 A; 1525 C; 1669 G; 1311 T; 0 U; 0 Other;	QY	TCGGTGTAGTTCGTTTCGCTCCAAAGCTGGGCTGTGTGACGAAACCCCGCTTACGCGGAC	1140
		DB		
		DB	TCGGTGTAGTTCGTTTCGCTCCAAAGCTGGGCTGTGTGACGAAACCCCGCTTACGCGGAC	1140
		QY	CGTGGCGCTTATCCGGTAACTATCGTCTTGTAGTCCAAACCGGTGAAGACACGACTTATCG	1200
		DB		
		DB	CGTGGCGCTTATCCGGTAACTATCGTCTTGTAGTCCAAACCGGTGAAGACACGACTTATCG	1200
		QY	CACTGGCAGCAGCTTCTACCATATCCCGATTAACCCAGCGAACCATTTCGAGGTGAT	1260
		DB		
		DB	CACTGGCAGCAGCTTCTACCATATCCCGATTAACCCAGCGAACCATTTCGAGGTGAT	1260
		QY	AGTTAAGATTATACCGAGGTATGAAAACGAGAAATTCGACCTTTACAGAAATTAATCTATGA	1320
		DB		
		DB	AGTTAAGATTATACCGAGGTATGAAAACGAGAAATTCGACCTTTACAGAAATTAATCTATGA	1320
		QY	AGCGCATATTTAAAGCTACCAAGCAGAGGATGAAGAGGATGAGAGGAGCAGATTG	1380
		DB		
		DB	AGCGCATATTTAAAGCTACCAAGCAGAGGATGAAGAGGATGAGAGGAGCAGATTG	1380
		QY	CCTTGAATATTTGACAACTACTGATAAGATAATACATCTTTTATAGAGATATCGCG	1440
		DB		
		DB	CCTTGAATATTTGACAACTACTGATAAGATAATACATCTTTTATAGAGATATCGCG	1440
		QY	TATGTAAAGATTTCAGGGGCAAGGCATAGGCGAGCGCTTATCAATATATCTATAGAAT	1500
		DB		
		DB	TATGTAAAGATTTCAGGGGCAAGGCATAGGCGAGCGCTTATCAATATATCTATAGAAT	1500
		QY	GGGCAAGCATAAAACTTTCGATGGAATAATGCTTGAACCCAGGACAATACTTATAG	1560
		DB		
		DB	GGGCAAGCATAAAACTTTCGATGGAATAATGCTTGAACCCAGGACAATACTTATAG	1560
		QY	CTTGTAAATTTACCAAAATTTGCTTTCAAAATCGGCTCCGCTCGATCTATGTTATACG	1620
		DB		
		DB	CTTGTAAATTTACCAAAATTTGCTTTCAAAATCGGCTCCGCTCGATCTATGTTATACG	1620
		QY	CCAACTTTGAAAAACAACTTTTGAAGAGCTGTTTCTGGTATTCTTAAGGTTTCTAGAAATGCA	1680

Query Match 94.3%; Score 4531.4; DB 4; Length 6017;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 4532; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB			
DB	1	CCGGGCTGGTGTGGCTCGCGCTGGGCTGGCGCGCTATGCTATGCTGCAAAACCGCGCAG	60
QY	61	AAACGCGGTGCGAGACACCGCGCGCGCGCTGTGATACCTCGCGG	120
DB			
DB	61	AAACGCGGTGCGAGACACCGCGCGCGCGCTGTGATACCTCGCGG	120
QY	121	AAACTTGGCCCTCACTGACAGATAGGGCGGACGTTGACACTTGAGGGCGGACTCAC	180
DB			
DB	121	AAAACTTGGCCCTCACTGACAGATAGGGCGGACGTTGACACTTGAGGGCGGACTCAC	180
QY	181	CCGGCGCGGCTTGAAGATGAGGGGAGGCTCGATTTTCGGCGCGGACGCTGGAGCTGGC	240
DB			
DB	181	CCGGCGCGGCTTGAAGATGAGGGGAGGCTCGATTTTCGGCGCGGACGCTGGAGCTGGC	240
QY	241	CAGCCTCGAAATCGCGGAAACCGCTGATTTTACGCGAGTTTCCACAGATGATGGA	300
DB			
DB	241	CAGCCTCGAAATCGCGGAAACCGCTGATTTTACGCGAGTTTCCACAGATGATGGA	300
QY	301	CAAGCCTGGGATAGTGCCTCGGTTATGACACTTGAGGGGCGGACTACTGACAGAT	360
DB			
DB	301	CAAGCCTGGGATAGTGCCTCGGTTATGACACTTGAGGGGCGGACTACTGACAGAT	360
QY	361	GAGGGGCGGATCTTGAACACTTGAAGGGGAGAGTGTGACAGATGAGGGGCGGACTAT	420
DB			
DB	361	GAGGGGCGGATCTTGAACACTTGAAGGGGAGAGTGTGACAGATGAGGGGCGGACTAT	420
QY	421	TGACATTTGAGGGGCTGTCCACAGGCGAGAAATCCAGCATTTTGAAGGGTTTCCGCGCGT	480
DB			
DB	421	TGACATTTGAGGGGCTGTCCACAGGCGAGAAATCCAGCATTTTGAAGGGTTTCCGCGCGT	480
QY	481	TTTTCGGCCACCGTAACTGTCTTTTAACTGCTTTTAAACCAATATTTATAAACCTTG	540
DB			
DB	481	TTTTCGGCCACCGTAACTGTCTTTTAACTGCTTTTAAACCAATATTTATAAACCTTG	540



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D 3841 AGCGTACCGCTCAAGCTGGAACCTTCCGCTTATGCGGATCGGATTCACCGCG 3900
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D 3901 TGAAGAGTGGCGGACAGCTGGCGAAGCTGCGAAGTTCGAGGAGCGGCTGG 3960
QY 3961 TGAACACGCTGGCTCAATGATGACCTGTGCTGCAACGCTAGGCGCTTGTGGGT 4020
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D 4081 CTGATGGCTGCTGATCAGTGGTGAATTTGTCGCGAGCTGCGGTCGGGAGCTGTT 4140
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D 4201 ACATTTGCGGAGCTTTTAACTGCTGCGGCTATCCCGGGGATATCATAGGCCG 4260
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D 4441 ATGATAATCATGCAAGACCGGCAACAGGATTCATCTTAAGAACTTTATTCGCAATG 4500
QY 4501 TTTGAAGATCGTTCGTCGAGCTATGGCCGA 4533
D 4501 TTTGAAGATCGTTCGTCGAGCTATGGCCGA 4533
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RESULT 9

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AAF80279
ID AAF80279 standard; DNA; 6017 BP.
XX
AC AAF80279;
XX
DT 29-JUN-2001 (first entry)
XX
DE Nucleotide sequence of plasmid pMR1121.
XX
KW Vector; transgenesis; trfA locus; RK2 ori; oriV; P285 protein;
KW P382 protein; antibiotic resistance gene; nptIII; transgenic plant; ss.
XX
OS Synthetic.
XX
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FT phosphotransferase and kanamycin resistance"
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FT and P382 enabling an increase in the replication rate"
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XX 03-SEP-1999; 99FR-00011112.
XX
XX (MERI-) MERISTEM THERAPEUTICS SA.
XX
XX Gruber V, Comeau D;
XX
XX WPI; 2001-359847/27.
XX
XX New vector free from non-essential elements, useful for transforming
XX cells for protein production and for preparing transgenic plants.
XX
XX Claim 20; Page 97-99; 180pp; French.
XX
XX The specification describes a synthetic vector containing only those
XX elements essential for its functionality and transgenesis of a cell
XX (especially a plant cell). The vector consists of at most one origin of
XX replication (ori), at most one sequence encoding a selection agent and a
XX trfA locus encoding a protein that increases the level of plasmid
XX replication. The vector particularly contains an RK2 ori, especially oriV
XX from PRK2 of Escherichia coli with a broad host range, an antibiotic
XX resistance gene (especially nptIII conferring resistance to kanamycin in
XX bacteria) and a trfA locus from PRK2 encoding the proteins P285 and P382.
XX The vectors are used to prepare transgenic plants and transformed host
XX cells for production of a heterologous proteins, e.g. insulin,
XX interferon, lipase, blood proteins and anti-inflammatory agents. The
XX present sequence represents a plasmid of the invention
XX
XX Sequence 6017 BP; 1513 A; 1525 C; 1669 G; 1310 T; 0 U; 0 Other;
XX
XX Query Match 94.3%; Score 4531.4; DB 4; Length 6017;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 4532; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CCGGGCTGGTGGCTCGCGCTGGCGGCTGCTATGCGCTTATGCGCTGCAACGCGCCAG 60
D 1 CCGGGCTGGTGGCTCGCGCTGGCGGCTGCTATGCGCTTATGCGCTGCAACGCGCCAG 60
QY 61 AAACGCGCTCGAAGCGCTGTGCGAGACACCGCGCGCGCGGCTTGTGATACCTCGCG 120
D 61 AAACGCGCTCGAAGCGCTGTGCGAGACACCGCGCGCGCGGCTTGTGATACCTCGCG 120
QY 121 AAACCTTGGCCCTCACTGACAGATGAGGGCGGAGCGTTGACACTTGTAGGGCGGACTCAC 180
D 121 AAACCTTGGCCCTCACTGACAGATGAGGGCGGAGCGTTGACACTTGTAGGGCGGACTCAC 180
```

Db 121 ABAACCTTGGCCCTCACTGACAGATGAGGGCGGAGCTTGACACTTGAGGGGCGCACTCAC 180  
Qy 181 CCGGCGGGCGTTGACAGATGAGGGCAGGCTCGAATTCGGCGCGGCGAGCGTGGAGCTGGC 240  
Db 181 CCGGCGGGCGTTGACAGATGAGGGCAGGCTCGAATTCGGCGCGGCGAGCGTGGAGCTGGC 240  
Qy 241 CAGCCTCGCAAAATCGGGAAGCGCCTGATTTTACGCGAGTGTTCGCCACAGATGATGGGA 300  
Db 241 CAGCCTCGCAAAATCGGGAAGCGCCTGATTTTACGCGAGTGTTCGCCACAGATGATGGGA 300  
Qy 301 CAAGCCTGGGGAATAAGTGCCTCGGTATTTGACACTTTGAGGGCGGCGACTACTGACAGAT 360  
Db 301 CAAGCCTGGGGAATAAGTGCCTCGGTATTTGACACTTTGAGGGCGGCGACTACTGACAGAT 360  
Qy 361 GAGGGCGCGATCCTTGACACTTTGAGGGCGAGAGTGTCTGACAGATGAGGGCGGCGACTAT 420  
Db 361 GAGGGCGCGATCCTTGACACTTTGAGGGCGAGAGTGTCTGACAGATGAGGGCGGCGACTAT 420  
Qy 421 TGACATTTGAGGGCTGTCCACAGGCAGAAATCCAGCAATTTGCAAGGGTTTCGCGCCGT 480  
Db 421 TGACATTTGAGGGCTGTCCACAGGCAGAAATCCAGCAATTTGCAAGGGTTTCGCGCCGT 480  
Qy 481 TTTTTCGGCCACCGCTAACCTGTCTTTTAACTGCTTTTAAACCAATATTTTAAACCTTG 540  
Db 481 TTTTTCGGCCACCGCTAACCTGTCTTTTAACTGCTTTTAAACCAATATTTTAAACCTTG 540  
Qy 541 TTTTAAACAGGGTGGCGCTGTGCGGTGACCGGCGACCGGAGGGGGGTGCGCCCC 600  
Db 541 TTTTAAACAGGGTGGCGCTGTGCGGTGACCGGCGACCGGAGGGGGGTGCGCCCC 600  
Qy 601 CTCTCGAACCCCTCCGGAAGGTATCGGCTGTGAATACCGCACAGATCGTAAGGAGA 660  
Db 601 CTCTCGAACCCCTCCGGAAGGTATCGGCTGTGAATACCGCACAGATCGTAAGGAGA 660  
Qy 661 AAATACCGCATCAGGCGCTCTTCGCTTCCTCGCTCACTGACTCGCTGCGTGGT 720  
Db 661 AAATACCGCATCAGGCGCTCTTCGCTTCCTCGCTCACTGACTCGCTGCGTGGT 720  
Qy 721 CCGCTGCGGAGCGGTATCAGCTCACTCAAGGCGGTAAATACGTTATCCACAGAAATCA 780  
Db 721 CCGCTGCGGAGCGGTATCAGCTCACTCAAGGCGGTAAATACGTTATCCACAGAAATCA 780  
Qy 781 GGGGATAACCGAGAAAGACATGTGAGCAAAAGCCAGCAAAAGCCAGGAACCGTAAA 840  
Db 781 GGGGATAACCGAGAAAGACATGTGAGCAAAAGCCAGCAAAAGCCAGGAACCGTAAA 840  
Qy 841 AAGCCCGCTTGTGCGGCTTTTCCATAGGCTCCGCGCCCTGACGAGCATCAAAAAAT 900  
Db 841 AAGCCCGCTTGTGCGGCTTTTCCATAGGCTCCGCGCCCTGACGAGCATCAAAAAAT 900  
Qy 901 CGAGCTCAAGTCAGAGTGGCGAAACCCGACAGGACTATAAGATACGAGGCGTTTCCC 960  
Db 901 CGAGCTCAAGTCAGAGTGGCGAAACCCGACAGGACTATAAGATACGAGGCGTTTCCC 960  
Qy 961 CCTGGAAGCTCCCTCGGCTCTCTGTTCCGACCTCGCGCTTACCGGATCCTGTC 1020  
Db 961 CCTGGAAGCTCCCTCGGCTCTCTGTTCCGACCTCGCGCTTACCGGATCCTGTC 1020  
Qy 1021 GCCTTTCTCCCTTCGGGAAGCGTGGCGTTTCTCATAGCTCACGCTGAGGTATCTCAGT 1080  
Db 1021 GCCTTTCTCCCTTCGGGAAGCGTGGCGTTTCTCATAGCTCACGCTGAGGTATCTCAGT 1080  
Qy 1081 TCGGTGATAGTTCGTTCCAGTGGCTGTGTGACGAAACCCCGGTTTACGCCCGAC 1140  
Db 1081 TCGGTGATAGTTCGTTCCAGTGGCTGTGTGACGAAACCCCGGTTTACGCCCGAC 1140  
Qy 1141 CGCTGCGCTTATCCGGTAACCTATCTGTTCCGACCTCAACCGGTAAAGACGACTATCG 1200  
Db 1141 CGCTGCGCTTATCCGGTAACCTATCTGTTCCGACCTCAACCGGTAAAGACGACTATCG 1200  
Qy 1201 CCACTGGCAGCAGCTTCTACATAAATCCGCGATAAACCAGCAACCATTTGAGGTGAT 1260  
Db 1201 CCACTGGCAGCAGCTTCTACATAAATCCGCGATAAACCAGCAACCATTTGAGGTGAT 1260

Qy 1261 AGGTAAGATTATACCGAGGTATGAAAAAGAGAAATTTGAACTTTTACAGAAATTTACTCTATGA 1320  
Db 1261 AGGTAAGATTATACCGAGGTATGAAAAAGAGAAATTTGAACTTTTACAGAAATTTACTCTATGA 1320  
Qy 1321 AGCGCCATATTTAAAAAGCTACCAAGACGAAGAGATGAAGAGATGAGAGGAGCAGATTG 1380  
Db 1321 AGCGCCATATTTAAAAAGCTACCAAGACGAAGAGATGAAGAGATGAGAGGAGCAGATTG 1380  
Qy 1381 CTTTGAATATATTGACAATACTGATAAGATAATACATCTTTTATATAGAGATATCGCCG 1440  
Db 1381 CTTTGAATATATTGACAATACTGATAAGATAATACATCTTTTATATAGAGATATCGCCG 1440  
Qy 1441 TATGTAAGATTTTACGGGGCAAGCATAGGAGCGCGCTTATCAATATATCTATAGAAT 1500  
Db 1441 TATGTAAGATTTTACGGGGCAAGCATAGGAGCGCGCTTATCAATATATCTATAGAAT 1500  
Qy 1501 GGGCAAGCATAAAACTTTGCAATGACTAAATGCTTGAACCCAGGACAATAACCTTATAG 1560  
Db 1501 GGGCAAGCATAAAACTTTGCAATGACTAAATGCTTGAACCCAGGACAATAACCTTATAG 1560  
Qy 1561 CTTGTAATTTTACCAAAATTTGGTTTCAAAATCGGCTCCGTCGATACTATGTTATACG 1620  
Db 1561 CTTGTAATTTTACCAAAATTTGGTTTCAAAATCGGCTCCGTCGATACTATGTTATACG 1620  
Qy 1621 CCAACTTTGAAAAACAATTTGAAAAAGCTGTTTTCTGGTATTTTAAAGTGTTTAGAAATGCAA 1680  
Db 1621 CCAACTTTGAAAAACAATTTGAAAAAGCTGTTTTCTGGTATTTTAAAGTGTTTAGAAATGCAA 1680  
Qy 1681 GGAACAGTGAATTTGGAGTTGCTTGTATATAATAGTCTTCTGGGATGATCTTTAAATACT 1740  
Db 1681 GGAACAGTGAATTTGGAGTTGCTTGTATATAATAGTCTTCTGGGATGATCTTTAAATACT 1740  
Qy 1741 GTAGAAAAAGGAGAAATATAAATGCTTAAATGCTTAAATGAGAAATATACCGGAAATTTGAAAAA 1800  
Db 1741 GTAGAAAAAGGAGAAATATAAATGCTTAAATGCTTAAATGAGAAATATACCGGAAATTTGAAAAA 1800  
Qy 1801 ACTGATCGAAAAATACCGCTGCTGTAAGAAATACCGAAGGAAATGCTCTCTCTAAGGTATA 1860  
Db 1801 ACTGATCGAAAAATACCGCTGCTGTAAGAAATACCGAAGGAAATGCTCTCTCTAAGGTATA 1860  
Qy 1861 TAAAGCTGGTGGGAGAAAACTATATTTTAAAAATGACGAGCAGCGGATATAAAGG 1920  
Db 1861 TAAAGCTGGTGGGAGAAAACTATATTTTAAAAATGACGAGCAGCGGATATAAAGG 1920  
Qy 1921 GACCACTATGATGTGGACGGGAAAGGACATGATGCTATGCTGGAAGGAAAGCTGCC 1980  
Db 1921 GACCACTATGATGTGGACGGGAAAGGACATGATGCTATGCTGGAAGGAAAGCTGCC 1980  
Qy 1981 TGTTCGAAAGGCTCTGCACCTTTGAAACGGCATGATGGCTGGAGCAATCTGCTCATGAGTGA 2040  
Db 1981 TGTTCGAAAGGCTCTGCACCTTTGAAACGGCATGATGGCTGGAGCAATCTGCTCATGAGTGA 2040  
Qy 2041 GGCAGATGGCGTCTTTTGTCTCGAAAGATGAAGATGAACAAAGCCCTGAAAAAGATTAT 2100  
Db 2041 GGCAGATGGCGTCTTTTGTCTCGAAAGATGAAGATGAACAAAGCCCTGAAAAAGATTAT 2100  
Qy 2101 CGAGCTGATGCGGAGTGCATCAGGCTCTTTTCACTCCATCGACATATCGGATTTGCCCTA 2160  
Db 2101 CGAGCTGATGCGGAGTGCATCAGGCTCTTTTCACTCCATCGACATATCGGATTTGCCCTA 2160  
Qy 2161 TACGAATAGCTTAGACAGCGCTTAGCCGAATTTGGATTACTTACTGAATAACGATCTGGC 2220  
Db 2161 TACGAATAGCTTAGACAGCGCTTAGCCGAATTTGGATTACTTACTGAATAACGATCTGGC 2220  
Qy 2221 CGATGTGGATTGCGAAAACTGGGAAAGAGACATCTCCATTTAAAGATCCGCGGAGCTGTA 2280  
Db 2221 CGATGTGGATTGCGAAAACTGGGAAAGAGACATCTCCATTTAAAGATCCGCGGAGCTGTA 2280  
Qy 2281 TGATTTTTTAAACCGGAAAGCCGGAAGGAACTTTGCTTTTCCACCGGACCTGGG 2340  
Db 2281 TGATTTTTTAAACCGGAAAGCCGGAAGGAACTTTGCTTTTCCACCGGACCTGGG 2340

QY	2341	AGACAGCAACATCTTTGTGAAAGATGCGAAAGTAAGTGGCTTTATTGATCTTCGGGAGAG	2400
Db	2341	AGACAGCAACATCTTTGTGAAAGATGCGAAAGTAAGTGGCTTTATTGATCTTCGGGAGAG	2400
QY	2401	CGGACGGCGGACAAAGTGGTATGACATCTGCTTCGCTCCGCTCGATCAGGAGGATAT	2460
Db	2401	CGGACGGCGGACAAAGTGGTATGACATCTGCTTCGCTCCGCTCGATCAGGAGGATAT	2460
QY	2461	CGGGGAAGAACAGTATGTCCAGCTATTTTGTGACTTACTGGGGATCAAGCCTGATTGGGA	2520
Db	2461	CGGGGAAGAACAGTATGTCCAGCTATTTTGTGACTTACTGGGGATCAAGCCTGATTGGGA	2520
QY	2521	GAAAAATAAATATATATTTTACTGATGAATTTGTTTAGTACTTAGATGTGGCGAAG	2580
Db	2521	GAAAAATAAATATATATTTTACTGATGAATTTGTTTAGTACTTAGATGTGGCGAAG	2580
QY	2581	ATCCCGGCGAAGAGGAGCGACCGACTTCTTCGCACTCAAGTGTGTTGGCTCTCAGG	2640
Db	2581	ATCCCGGCGAAGAGGAGCGACCGACTTCTTCGCACTCAAGTGTGTTGGCTCTCAGG	2640
QY	2641	CCGAGGCCCAACGCAAGTATTTGGGCAAGGGGTGCGTGGTATTTCTGTCAGGGCAAGATTC	2700
Db	2641	CCGAGGCCCAACGCAAGTATTTGGGCAAGGGGTGCGTGGTATTTCTGTCAGGGCAAGATTC	2700
QY	2701	GGAATACCAAGTACGAGAGGACCGCCAGACGTCTACCGGACCGACTTCAATTCGCGATA	2760
Db	2701	GGAATACCAAGTACGAGAGGACCGCCAGACGTCTACCGGACCGACTTCAATTCGCGATA	2760
QY	2761	AGGTGATTTATCTGGACACCAAGGACCAAGGCGGTCGAATCAGGAATAGGGCAATTG	2820
Db	2761	AGGTGATTTATCTGGACACCAAGGACCAAGGCGGTCGAATCAGGAATAGGGCAATTG	2820
QY	2821	CCCCGGCGTGAAGTCCGCGCAAGAGGGTGAATGAATCGGACGTTTGTACCGGA	2880
Db	2821	CCCCGGCGTGAAGTCCGCGCAAGAGGGTGAATGAATCGGACGTTTGTACCGGA	2880
QY	2881	AGGCATACAGGCAAGAACTGATCGACGCGGGTTCGCGGAGGATGCGAAACCATCG	2940
Db	2881	AGGCATACAGGCAAGAACTGATCGACGCGGGTTCGCGGAGGATGCGAAACCATCG	2940
QY	2941	CAAGCCGACCGTATCGCTGCGCCCGCGGAACCTTCAGTCCGTCGGCTCGATGGTCC	3000
Db	2941	CAAGCCGACCGTATCGCTGCGCCCGCGGAACCTTCAGTCCGTCGGCTCGATGGTCC	3000
QY	3001	AGCAAGTACGGCAAGAACTGATCGACGCGGACAGCGTGCACCTGGCTCCCGCTCCCGG	3060
Db	3001	AGCAAGTACGGCAAGAACTGATCGACGCGGACAGCGTGCACCTGGCTCCCGCTCCCGG	3060
QY	3061	CGCCATCGGCGCGTGGAGCGTTCGCTCGAACAGGAGGCGGAGGTTTGGCGA	3120
Db	3061	CGCCATCGGCGCGTGGAGCGTTCGCTCGAACAGGAGGCGGAGGTTTGGCGA	3120
QY	3121	AGTCGATGACCATCGACCGGAGGAACTATGACGACCAAGAGCGAAACCGCGCGG	3180
Db	3121	AGTCGATGACCATCGACCGGAGGAACTATGACGACCAAGAGCGAAACCGCGCGG	3180
QY	3181	AGGACCTGCAAAACAGGTGAGGAGCGCAAGCAGGCGCGTTCGTAACACACCAAGC	3240
Db	3181	AGGACCTGCAAAACAGGTGAGGAGCGCAAGCAGGCGCGTTCGTAACACACCAAGC	3240
QY	3241	AGCAGATCAAGGAAATGCAAGTTCCTTGTTCGATATTCGCGCGTGGCGGACCGATGC	3300
Db	3241	AGCAGATCAAGGAAATGCAAGTTCCTTGTTCGATATTCGCGCGTGGCGGACCGATGC	3300
QY	3301	GAGCGATGCCAAACGACGCGCGCTCTGCGCTGTTTCAACGCGGCAACAGAAATCC	3360
Db	3301	GAGCGATGCCAAACGACGCGCGCTCTGCGCTGTTTCAACGCGGCAACAGAAATCC	3360
QY	3361	CGCGGAGGCGCTGCAAAACAGGTGCAATTTTCCAGCTCAACAGGACGTGAAGATCACCT	3420
Db	3361	CGCGGAGGCGCTGCAAAACAGGTGCAATTTTCCAGCTCAACAGGACGTGAAGATCACCT	3420
QY	3421	ACACCGGCGTTCGAGCTGCGGGCGGACGATGACGAACTGTTGGTGGCAGCAGGTTTGGAGT	3480

Db	3421	ACACCGGCGTTCGAGCTGCGGGCGGACGATGACGAACTGGTGTGSCAGCAGGTTTGGAGT	3480
QY	3481	ACGCGAAGCGCACCCCTATTCGCGGAGCCGATCACCTTTCAGTTCTACGAGCTTTGCCAGG	3540
Db	3481	ACGCGAAGCGCACCCCTATTCGCGGAGCCGATCACCTTTCAGTTCTACGAGCTTTGCCAGG	3540
QY	3541	ACTGCGGCTGGTCGATCAATGCGCGGTATTTACAGAAAGCCGAGGAATGCTCTCGCGCC	3600
Db	3541	ACTGCGGCTGGTCGATCAATGCGCGGTATTTACAGAAAGCCGAGGAATGCTCTCGCGCC	3600
QY	3601	TACAGCGACGCGGATGGGCTTCACGTCGACCGGCTTGGGACCTTGGGAATCGGTGTGCG	3660
Db	3601	TACAGCGACGCGGATGGGCTTCACGTCGACCGGCTTGGGACCTTGGGAATCGGTGTGCG	3660
QY	3661	TGCTGCACCGCTTTCGCGCTCTCGGACCGTGGCAAGAAACGTCCTGTCAGGCTCTGA	3720
Db	3661	TGCTGCACCGCTTTCGCGCTCTCGGACCGTGGCAAGAAACGTCCTGTCAGGCTCTGA	3720
QY	3721	TGACGAGGAAATCGTCTGCTGTTTGTGCGGACCACTACAGAAATTCATATGGGAGA	3780
Db	3721	TGACGAGGAAATCGTCTGCTGTTTGTGCGGACCACTACAGAAATTCATATGGGAGA	3780
QY	3781	AGTACCGCAAGCTGTCCGCGACGCGCCGACGGATGTTTTCAGTTCGACCTCGCACCGGG	3840
Db	3781	AGTACCGCAAGCTGTCCGCGACGCGCCGACGGATGTTTTCAGTTCGACCTCGCACCGGG	3840
QY	3841	AGCGGTACCGCTCAAGCTGGAAACCTTCCGCTCATGTGCGGATTCGAGTTCCACCGCG	3900
Db	3841	AGCGGTACCGCTCAAGCTGGAAACCTTCCGCTCATGTGCGGATTCGAGTTCCACCGCG	3900
QY	3901	TGAAGAAAGTGGCGCGACGAGTGGCGAAGCCTCGAAGAGTTTGCAGGCGAGCGGCTGG	3960
Db	3901	TGAAGAAAGTGGCGCGACGAGTGGCGAAGCCTCGAAGAGTTTGCAGGCGAGCGGCTGG	3960
QY	3961	TGGAACACGCTTGGGTCAATGATGACCTCGGTGCAATTTGCAAAACGCTAGGGCTTTGGGGT	4020
Db	3961	TGGAACACGCTTGGGTCAATGATGACCTCGGTGCAATTTGCAAAACGCTAGGGCTTTGGGGT	4020
QY	4021	CAGTTCCGCTGGGGTTCAGCAGCAGCGCTTACTGCGCATTTCTAGCTTCAGCTTCCT	4080
Db	4021	CAGTTCCGCTGGGGTTCAGCAGCAGCGCTTACTGCGCATTTCTAGCTTCAGCTTCCT	4080
QY	4081	CTGATGGGCTGCTGATCGAGTGGTGTATTTGTGCGGAGCTGCGGCGGAGCTGTT	4140
Db	4081	CTGATGGGCTGCTGATCGAGTGGTGTATTTGTGCGGAGCTGCGGCGGAGCTGTT	4140
QY	4141	GGTGGCTGGTGGCAGGATATATTTGGTGTGTAACAAATTTGACGCTTAGACAACTTAATA	4200
Db	4141	GGTGGCTGGTGGCAGGATATATTTGGTGTGTAACAAATTTGACGCTTAGACAACTTAATA	4200
QY	4201	ACACATTCGCGACGTTTTTAATGTAAGTGGGCTATCCCCCGGGGATATCCATAGGCCCG	4260
Db	4201	ACACATTCGCGACGTTTTTAATGTAAGTGGGCTATCCCCCGGGGATATCCATAGGCCCG	4260
QY	4261	ATCTAGTAACATAATGACACCGCGCGGATAATTTATCTAGTTTTCGCGCTATATTTTG	4320
Db	4261	ATCTAGTAACATAATGACACCGCGCGGATAATTTATCTAGTTTTCGCGCTATATTTTG	4320
QY	4321	TTTTCTATCGCGTATTAATGTAATTTGCGGAGCTTAATCATAAAAACCCATCTCAT	4380
Db	4321	TTTTCTATCGCGTATTAATGTAATTTGCGGAGCTTAATCATAAAAACCCATCTCAT	4380
QY	4381	AATAAGCTCATGATGATGTAATTTATGATGCTTAACGTAATTCACAGAAATAT	4440
Db	4381	AATAAGCTCATGATGATGTAATTTATGATGCTTAACGTAATTCACAGAAATAT	4440
QY	4441	ATGATAATCATCGCAAGACCGGCAACAGGATTCATTTTAAAGAACTTTTATGCGGAAATG	4500
Db	4441	ATGATAATCATCGCAAGACCGGCAACAGGATTCATTTTAAAGAACTTTTATGCGGAAATG	4500
QY	4501	TTTGAACGATCGTTCGTGAGCTATGGGCCGA 4533	

Db 4501 TTTGAACGATCGTTCTCGAGCTATGGGCCAA 4533

RESULT 10

AAF80282

ID AAF80282 standard; DNA; 6767 BP.

XX AAF80282;

AC AAF80282;

XX 29-JUN-2001 (first entry)

DT

XX Nucleotide sequence of plasmid pMRT1175.

DE

XX Vector; transgenesis; trfA locus; RK2 ori; oriV; P285 protein;

KW P382 protein; antibiotic resistance gene; nptIII; transgenic plant; ss.

KW

XX Synthetic.

OS

XX

FH Key Location/Qualifiers

FT rep\_origin 1..654

FT /\*tag= a

FT /note= "ori RK2"

FT

FT rep\_origin 655..1263

FT /\*tag= b

FT /note= "ori Cole1"

FT CDS 1264..2603

FT /\*tag= c

FT /note= "NPT III gene coding for neomycin

FT phosphotransferase and kanamycin resistance"

FT CDS 2604..4098

FT /\*tag= d

FT /note= "trfA locus from RK2 coding for two proteins P285

FT and P382 enabling an increase in the replication rate"

FT misc\_feature 4106..4271

FT /\*tag= e

FT /note= "T-DNA left border"

FT terminator 4272..4559

FT /\*tag= f

FT /note= "nopaline synthetase terminator"

FT CDS 4559..5556

FT /\*tag= g

FT /note= "NPT III gene coding for neomycin

FT phosphotransferase and kanamycin resistance"

FT promoter 5557..5771

FT /\*tag= h

FT /note= "nopaline synthetase promoter"

FT polyA\_signal 5830..6560

FT /\*tag= i

FT /note= "polyA from 35S ribosome"

FT misc\_feature 6587..6760

FT /\*tag= j

FT /note= "T-DNA right border"

XX

PN FR2798139-A1.

XX

XX 09-MAR-2001.

XX

XX 03-SEP-1999; 99FR-00011112.

XX

XX 03-SEP-1999; 99FR-00011112.

XX (MERI-) MERISTEM THERAPEUTICS SA.

XX

XX Gruber V, Comeau D;

XX

XX WPI: 2001-259847/27.

DR

XX New vector free from non-essential elements, useful for transforming

FT cells for protein production and for preparing transgenic plants.

XX

XX Claim 20; Page 108-110; 180pp; French.

PS

XX The specification describes a synthetic vector containing only those

CC

CC elements essential for its functionality and transgenesis of a cell

CC (especially a plant cell). The vector consists of at most one origin of

CC replication (ori), at most one sequence encoding a selection agent and a

CC trfA locus encoding a protein that increases the level of plasmid

CC replication. The vector particularly contains an RK2 ori, especially oriv

CC from PRK2 of Escherichia coli with a broad host range, an antibiotic

CC resistance gene (especially nptIII conferring resistance to kanamycin in

CC bacteria) and a trfA locus from PRK2 encoding the proteins P285 and P382.

CC The vectors are used to prepare transgenic plants and transformed host

CC cells for production of a heterologous proteins, e.g. insulin.

CC interferon, lipase, blood proteins and anti-inflammatory agents. The

CC present sequence represents a plasmid of the invention

XX

SQ Sequence 6767 BP; 1762 A; 1675 C; 1821 G; 1509 T; 0 U; 0 Other;

Query Match 94.3%; Score 4531.4; DB 4; Length 6767;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 4532; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCGGGCTGGTTGCCCTCGCGCTGGCTGGCGCGCTGTATGCCCTGCAACGCCGCCAG 60

DB |||||

QY 1 CCGGGCTGGTTGCCCTCGCGCTGGCGCGCTGTATGCCCTGCAACGCCGCCAG 60

DB |||||

QY 61 AAACGCGGTGAAAGCGGTGTGGAGACACCGCGCGCGCGGTGTGGATACCTCGCG 120

DB |||||

QY 61 AAACGCGGTGAAAGCGGTGTGGAGACACCGCGCGCGCGGTGTGGATACCTCGCG 120

DB |||||

QY 121 AAACCTTGCCCTCACTGACAGATGAGGGCGGACGTTGACACTTGAGGGCGGACTCAC 180

DB |||||

QY 121 AAACCTTGCCCTCACTGACAGATGAGGGCGGACGTTGACACTTGAGGGCGGACTCAC 180

DB |||||

QY 181 CCGGGCGCGGTGACAGATGAGGGCGGCTCGATTTCCGCGCGGACGCTGGAGCTGGC 240

DB |||||

QY 181 CCGGGCGCGGTGACAGATGAGGGCGGCTCGATTTCCGCGCGGACGCTGGAGCTGGC 240

DB |||||

QY 241 CAGCCTCGCAAAATCGGCGAAACGCTGATTTTACCGGAGTTTCCACAGATGATGGA 300

DB |||||

QY 241 CAGCCTCGCAAAATCGGCGAAACGCTGATTTTACCGGAGTTTCCACAGATGATGGA 300

DB |||||

QY 301 CAAGCTGGGGATAAGTGGCTTGTGACACTTTGAGGGCGGCGGACTTACTGACAGAT 360

DB |||||

QY 301 CAAGCTGGGGATAAGTGGCTTGTGACACTTTGAGGGCGGCGGACTTACTGACAGAT 360

DB |||||

QY 361 GAGGGCGGATCCTTTGACACTTTGAGGGCGGAGTGTGACAGATGAGGGCGGCGGACTTAT 420

DB |||||

QY 361 GAGGGCGGATCCTTTGACACTTTGAGGGCGGAGTGTGACAGATGAGGGCGGCGGACTTAT 420

DB |||||

QY 421 TGACATTTGAGGGGCTGTCACAGGAGAGAAATCCAGACTTTTCAAGGGTTTCGCGCGT 480

DB |||||

QY 421 TGACATTTGAGGGGCTGTCACAGGAGAGAAATCCAGACTTTTCAAGGGTTTCGCGCGT 480

DB |||||

QY 481 TTTTCGGCCACCGCTAACCTGTCTTTTAACTGCTTTTAAACCAATATTTTAAACCTTG 540

DB |||||

QY 481 TTTTCGGCCACCGCTAACCTGTCTTTTAACTGCTTTTAAACCAATATTTTAAACCTTG 540

DB |||||

QY 541 TTTTAAACCGAGGCTGCGCGCTGTCGCGGACCGCGGACCGAGGGGGTCCCGCCC 600

DB |||||

QY 541 TTTTAAACCGAGGCTGCGCGCTGTCGCGGACCGCGGACCGAGGGGGTCCCGCCC 600

DB |||||

QY 601 CTTCTCGAACCTTCCCGGAAAGGTATGCGGTGTGAATACCGACAGATCGTAAGAGA 660

DB |||||

QY 601 CTTCTCGAACCTTCCCGGAAAGGTATGCGGTGTGAATACCGACAGATCGTAAGAGA 660

DB |||||

QY 661 AAATACCGATCAGGGGCTCTTCGGTCTCTCGCTCTACTGCTGCGCTCGGTCGTT 720

DB |||||

QY 661 AAATACCGATCAGGGGCTCTTCGGTCTCTCGCTCTACTGCTGCGCTCGGTCGTT 720

DB |||||

QY 721 CGGCTCGGCGAGCGGTATCAGCTCACTAAAGCGGTATACGTTTATCCACAGATCA 780

DB |||||

QY 721 CGGCTCGGCGAGCGGTATCAGCTCACTAAAGCGGTATACGTTTATCCACAGATCA 780

DB |||||

QY 781 GGGGATTAACGAGGAAAGAAATGTGAGCAAAAGGGCCAGCAAAAGCGGAGAACCGTAAA 840

DB |||||



Db 781 GGGGATAACCCAGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGGTAAA 840  
Qy 841 AAGCCCGCGTGTGCGCGTTTTTCCATAGCTCTCGGCCCTCGACGAGCATCACAAAAAT 900  
Db 841 AAGCCCGCGTGTGCGCGTTTTTCCATAGCTCTCGGCCCTCGACGAGCATCACAAAAAT 900  
Qy 901 CGACGCTCAAGTCAGAGGTGGGAAACCCGACAGGACTATAAAGATACACAGGCGTTTCCC 960  
Db 901 CGACGCTCAAGTCAGAGGTGGGAAACCCGACAGGACTATAAAGATACACAGGCGTTTCCC 960  
Qy 961 CTTGGAAGCTCCCTCGTGCCTCTCTGTTTCCGACCTCGCGTTACCGATACCTGTCC 1020  
Db 961 CTTGGAAGCTCCCTCGTGCCTCTCTGTTTCCGACCTCGCGTTACCGATACCTGTCC 1020  
Qy 1021 GCCTTTCTCCCTTCGGGAAGCGTGGCGTTTTCTCATAGCTCACGCTGTAGGTATCTCAGT 1080  
Db 1021 GCCTTTCTCCCTTCGGGAAGCGTGGCGTTTTCTCATAGCTCACGCTGTAGGTATCTCAGT 1080  
Qy 1081 TCGGTGTAGTGTGCTCGCTCAAGCTGGGCTGTGTGCAAGAACCCCGCTTACGCCGAC 1140  
Db 1081 TCGGTGTAGTGTGCTCGCTCAAGCTGGGCTGTGTGCAAGAACCCCGCTTACGCCGAC 1140  
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Db 1141 CGCTGCGCCTTATCCGCTCAACTATCGTCTTGTAGTCCAAACCCGTAAGACACGACTTATCG 1200  
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Db 1201 CCACTGGCAGCAGCCTTCTACCAATAATCCGCGATAAACCAGCGAACCAATTTGAGGTGAT 1260  
Qy 1261 AGTAAAGATTATCCGAGGTATGAAAACGAGAAATCGACCTTTACAGAAATTAATCTCTATGA 1320  
Db 1261 AGTAAAGATTATCCGAGGTATGAAAACGAGAAATCGACCTTTACAGAAATTAATCTCTATGA 1320  
Qy 1321 AGCCGCATATTTAAAAGCTTACCAACGAGAGGATGAAGAGTGAAGAGGATGAGGAGGAGATG 1380  
Db 1321 AGCCGCATATTTAAAAGCTTACCAACGAGAGGATGAAGAGTGAAGAGGATGAGGAGGAGATG 1380  
Qy 1381 CTTTGAATATATTGACAACTACTGATAAGATAATACATCTTTTATAGAAAGATATCGCG 1440  
Db 1381 CTTTGAATATATTGACAACTACTGATAAGATAATACATCTTTTATAGAAAGATATCGCG 1440  
Qy 1441 TATGTAAAGATTTCAGGGGCAAGGATAGGACGCGCTTATCAATATATCTATAGAAT 1500  
Db 1441 TATGTAAAGATTTCAGGGGCAAGGATAGGACGCGCTTATCAATATATCTATAGAAT 1500  
Qy 1501 GGGCAAGCATAAAACCTTGCACTGGAATAATGCTTGAACCCGAGGACNAATACCTTATAG 1560  
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Db 1741 GTAGAAAAGGAAGAAATATAAATGCTTAAAATGAGAATATCACCGGAATTTGAAAAA 1800  
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Db 1801 ACTGATCGAAAAATACCGCTGCGTAAAAGATACGGAAGGAATGTCCTCTGCTAAAGGTATA 1860  
Qy 1861 TAACTGTGGGAGAAAATGAAAACTTATATTTAAAAATGACGACAGCCGCTATAAAGG 1920  
Db 1861 TAACTGTGGGAGAAAATGAAAACTTATATTTAAAAATGACGACAGCCGCTATAAAGG 1920

Qy

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Db |||||
QY 4501 TTTGAAACGATCGTTCGTCGAGCTATGGGCCCGA 4533
Db |||||

RESULT 11
AAF80287
ID AAF80287 standard; DNA; 6865 BP.
XX
AC AAF80287;
XX
XX 29-JUN-2001 (first entry)
XX
DE Nucleotide sequence of plasmid pMR1195.
XX
KW Vector; transgenesis; trfA locus; RK2 ori; nptIII; P285 protein;
KW P382 protein; antibiotic resistance gene; nptIII; transgenic plant; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT rep_origin 1..654
FT /tag= a
FT /note= "ori RK2"
FT 655..1263
FT /tag= b
FT /note= "ori Cole1"
FT 1264..2603
FT /tag= c
FT /note= "npt III gene coding for neomycin
FT phosphotransferase and kanamycin resistance"
FT 2604..4098
FT /tag= d
FT /note= "T-rfA locus from RK2 coding for two proteins P285
FT and P382 enabling an increase in the replication rate"
FT 4106..4271
FT misc_feature /tag= e
FT /note= "T-DNA left border"
FT 4272..4559
FT terminator /tag= f
FT /note= "nopaline synthetase terminator"
FT 4575..5150
FT CDS /tag= g
FT /note= "Bar gene coding for phosphotricin
FT acetyltransferase and glufosinate resistance"
FT 5174..5685
FT intron
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Db 1441 TATGTAAGGATTTTCAGGGGCGAAGGCATAGCAGCGCGCTTATCAATATATATCTATAGAAT 1500  
Qy 1501 GGGCAAAAGCAATAAACTTGATGACTAATGCTTGAAACCCAGGACAAATAACCTTATAG 1560  
Db 1501 GGGCAAAAGCAATAAACTTGATGACTAATGCTTGAAACCCAGGACAAATAACCTTATAG 1560  
Qy 1561 CTTGTAAATTTCTACCAAAATTTGTTTCAAAATCGGCTCGGTGATACCTATGTTATACG 1620  
Db 1561 CTTGTAAATTTCTACCAAAATTTGTTTCAAAATCGGCTCGGTGATACCTATGTTATACG 1620  
Qy 1621 CCAACTTTGAAAACAACTTTGAAAAGCTGTTTTCTCGTATTTAAAGTTTTAGAAATGCAA 1680  
Db 1621 CCAACTTTGAAAACAACTTTGAAAAGCTGTTTTCTCGTATTTAAAGTTTTAGAAATGCAA 1680  
Qy 1681 GGAACAGTGAATTTGGAGTTCGTCTTGTTATTAATTAATTAATTAATTAATTAATTAATTAAT 1740  
Db 1681 GGAACAGTGAATTTGGAGTTCGTCTTGTTATTAATTAATTAATTAATTAATTAATTAATTAAT 1740  
Qy 1741 GTAGAAAAGGAGGAATAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1800  
Db 1741 GTAGAAAAGGAGGAATAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1800  
Qy 1801 ACTGATCGAAAAATACCGCTGCGTAAAGATACGAAAGGAATGTCTCTGCTAAAGGTATA 1860  
Db 1801 ACTGATCGAAAAATACCGCTGCGTAAAGATACGAAAGGAATGTCTCTGCTAAAGGTATA 1860  
Qy 1861 TAAGCTGGTGGGAGAAAATGAAAACCTATATTTAAAAATGACGACACGCCGGTATAAAGG 1920  
Db 1861 TAAGCTGGTGGGAGAAAATGAAAACCTATATTTAAAAATGACGACACGCCGGTATAAAGG 1920  
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Db 1921 GACCACTATGATGTGAACGGGAAGGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1980  
Qy 1981 TGTTCAAAAGGCTCTGCACTTTGAAACGCGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2040  
Db 1981 TGTTCAAAAGGCTCTGCACTTTGAAACGCGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2040  
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Db 2041 GGGCGATGGGCTCTTTGCTCGGAAGAGATGAAGAGATGAACAAAGCCCTGAAAAGATTAT 2100  
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Db 2101 CGAGCTGTATCGGAGTGCATCAGGCTTTTCACTCCATCGACATATCGGATTTGCCCTA 2160  
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Db 2281 TGATTTTTTAAAGACGGAAAGCCGAGAGAACTTGTCTTTTCCACCGCGACCTGGG 2340  
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Qy 2401 CGGAGGCGGACAAAGTGGTATGACATTTGCTTTCTGGTCCGGTTCGATCAGGGAAGGATAT 2460  
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Qy 2461 CGGGGAAGACACTATGTCGAGCTATTTTTCATCTACTCGGGATCAAGCTGATTTGGGA 2520  
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Db 2521 GAAAATAAAATATTTATTTTACTGGATGAATTTTGTAGTACCTAGATGTGGCGCAACG 2580

Qy 2581 ATCCCGCGACAGCAGGAGCGCACCGACTTCTTCCGCATCAAGTGTGTTTGGCTCTCAGG 2640  
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Qy 2701 GGAATACCAAGTACGAGAAAGGACGCGCAGACGGTCTTACGGGACCGACTTCAATTTGCCGATA 2760  
Db 2701 GGAATACCAAGTACGAGAAAGGACGCGCAGACGGTCTTACGGGACCGACTTCAATTTGCCGATA 2760  
Qy 2761 AGTGTGATTTCTGGACACCAAGGACACGAGCGGGTCAATCAGGAATTAAGGCACATTCG 2820  
Db 2761 AGTGTGATTTCTGGACACCAAGGACACGAGCGGGTCAATCAGGAATTAAGGCACATTCG 2820  
Qy 2821 CCCCGGCTGAGTTCGGGGCAATCCCAGCAAGGAGGGTGAATGAATCGGACGTTTTGACCGGA 2880  
Db 2821 CCCCGGCTGAGTTCGGGGCAATCCCAGCAAGGAGGGTGAATGAATCGGACGTTTTGACCGGA 2880  
Qy 2881 AGGCATACAGGCAAGAACTGATCGACCGGGGTTTTCCGCGAGGATGCCGAAACCATTCG 2940  
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Qy 3301 GAGGATGCCAAAGCAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3360  
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Query Match 94.3%; Score 4531.4; DB 4; Length 7503; Best Local Similarity 100.0%; Pred. No. 0; Matches 4532; Conservative 0; Mismatches 1; Indels 0; Gaps 0;									
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Db	1	CCGGGCTGGTTCGGCTCGCGCTGGGCTGGCGGCGCTCTATGGCCCTGCAAGCGCCAG	60						
Qy	61	AAACGCGCTGAAGCCGTGTGCGAGACAACCGCGGCGCGCGGTGTGAGATACCTCGCGG	120						
Db	61	AAACGCGCTGAAGCCGTGTGCGAGACAACCGCGGCGCGCGGTGTGAGATACCTCGCGG	120						
Qy	121	AAACCTGGCCCTCACATGACAGATGAGGGCGGACGTTGACACTTGAGGGGCGGACCTAC	180						
Db	121	AAACCTGGCCCTCACATGACAGATGAGGGGCGGACGTTGACACTTGAGGGGCGGACCTAC	180						
Qy	181	CCGGCGCGGCTTGACAGATGAGGGCGAGGCTCGATTTCCGCGCGCGACGTGGAGCTGGC	240						
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Qy	241	CAGCCTCGCAAAATCGGCGAAAAACCCCTGATTTTACGCGAGTTTCCCAACAGATGATGGA	300						
Db	241	CAGCCTCGCAAAATCGGCGAAAAACCCCTGATTTTACGCGAGTTTCCCAACAGATGATGGA	300						
Qy	301	CAAGCCTGGGGATAAAGTGCCTCGGCTATTGACACTTTGAGGGGCGGACCTACTGACAGAT	360						
Db	301	CAAGCCTGGGGATAAAGTGCCTCGGCTATTGACACTTTGAGGGGCGGACCTACTGACAGAT	360						
Qy	361	GAGGGCGCGATCCTTGACACTTGAGGGCGAGGCTGCTGACAGATGAGGGGCGCACCTAT	420						
Db	361	GAGGGCGCGATCCTTGACACTTGAGGGCGAGGCTGCTGACAGATGAGGGGCGCACCTAT	420						
Qy	421	TGACATTTGAGGGCTGTGACAGGCAAAATCCAGCATTTGCAAGGGTTTCGCGCCGT	480						
Db	421	TGACATTTGAGGGCTGTGACAGGCAAAATCCAGCATTTGCAAGGGTTTCGCGCCGT	480						
Qy	481	TTTTTGGGCCACCGCTAACCTGTCTTTTAACTGCTTTTAAACCAATTTTATAAACCTTG	540						
Db	481	TTTTTGGGCCACCGCTAACCTGTCTTTTAACTGCTTTTAAACCAATTTTATAAACCTTG	540						
Qy	541	TTTTTAAACCGGCTGCGCCCTGTGCGGTGACCGCGCACCGCGAGGGGGTTCGCCCCC	600						
Db	541	TTTTTAAACCGGCTGCGCCCTGTGCGGTGACCGCGCACCGCGAGGGGGTTCGCCCCC	600						
Qy	601	CTTCTCGAAACCCCTCCGGAAGGTATGCGGTGTAATAACCGACAGATGCGTGAAGAGA	660						
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Qy	661	AAATACCGCATCAGGCGCTCTTCCGCTTCTCGCTCACTGACTCGCTCGCTCGCTCGTT	720						
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Db	721	CGGCTGGCGGAGCGGTATCAGCTCACTCAAAGCGGTAAATACGGTTATCCACAGAAATCA	780						
Qy	781	GGGATAAACCGAGAAAGAACATGTGACAAAAGGCGAGCAAAAAGGCGGAAACCGTAAA	840						
Db	781	GGGATAAACCGAGAAAGAACATGTGACAAAAGGCGAGCAAAAAGGCGGAAACCGTAAA	840						
Qy	841	AAGGCGCGGTTGCTGGCGTTTTTCCATAGGCTCCGCCCTCGACGAGCATCAAAAAT	900						
Db	841	AAGGCGCGGTTGCTGGCGTTTTTCCATAGGCTCCGCCCTCGACGAGCATCAAAAAT	900						
Qy	901	CGACGCTCAAGTCAGAGTGGCGAAACCCGACAGGACTATAAAGATACCGGCGGTTTCCC	960						
Db	901	CGACGCTCAAGTCAGAGTGGCGAAACCCGACAGGACTATAAAGATACCGGCGGTTTCCC	960						
Qy	961	CCTGGAGCTCCCTCGTGGCTCTCTCTGTTCCGACCTGCGCGCTTACCGGATACCTGTCC	1020						
Db	961	CCTGGAGCTCCCTCGTGGCTCTCTCTGTTCCGACCTGCGCGCTTACCGGATACCTGTCC	1020						
Qy	1021	GCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGT	1080						

Db	1021	GCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGT	1080						
Qy	1081	TCGGTGTAGGTGCTTCGCTCCAAAGCTGGGCTGTGTGCAAGAACCCCGGTTAGGCCGAC	1140						
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Qy	1141	CGCTGCGCTTATCCGGTAACCTATCGTCTTGAGTCCAAACCCCGTAAGACACGACTTATCG	1200						
Db	1141	CGCTGCGCTTATCCGGTAACCTATCGTCTTGAGTCCAAACCCCGTAAGACACGACTTATCG	1200						
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Qy	1261	AGTAAAGATTTATCCGAGGTATGAAAACGAGAAATTCGACCTTTACAGAAATTTACTCTATGA	1320						
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Qy	1321	AGCGCCATATTTAAAAGCTTACCAAGCAAGAGGATGAAGAGCATGAGGAGGACAGATTG	1380						
Db	1321	AGCGCCATATTTAAAAGCTTACCAAGCAAGAGGATGAAGAGCATGAGGAGGACAGATTG	1380						
Qy	1381	CCTTGAATATATTGACAATACTGATTAAGATAATACATCTTTTATATAGAGATATCGCCG	1440						
Db	1381	CCTTGAATATATTGACAATACTGATTAAGATAATACATCTTTTATATAGAGATATCGCCG	1440						
Qy	1441	TATGTAAGATTTACGGGGCAAGGATAGGACGCGGCTTATCAATATATCTATAGAAAT	1500						
Db	1441	TATGTAAGATTTACGGGGCAAGGATAGGACGCGGCTTATCAATATATCTATAGAAAT	1500						
Qy	1501	GGCAAGGATATAAACTTGCATGAGTAATGCTTGAACCCAGGACAAATAACCTTATAG	1560						
Db	1501	GGCAAGGATATAAACTTGCATGAGTAATGCTTGAACCCAGGACAAATAACCTTATAG	1560						
Qy	1561	CTTGTAAATTTTACCAAAATTTGGTTTCAAAATTCGGCTCCGTCGATATGTTATACG	1620						
Db	1561	CTTGTAAATTTTACCAAAATTTGGTTTCAAAATTCGGCTCCGTCGATATGTTATACG	1620						
Qy	1621	CGAATTTGAAAACAACTTTGAAAAGCTGTTTTCTGGTATTTTAAAGTTTAAAGTGC	1680						
Db	1621	CGAATTTGAAAACAACTTTGAAAAGCTGTTTTCTGGTATTTTAAAGTTTAAAGTGC	1680						
Qy	1681	GGAAAGTGAATTTGGAGTTTCGCTTGTATAATTTAGCTTCTGGGGTATCTTTAAATACT	1740						
Db	1681	GGAAAGTGAATTTGGAGTTTCGCTTGTATAATTTAGCTTCTGGGGTATCTTTAAATACT	1740						
Qy	1741	GTAGAAAAGAGGAAGGAAATAATAATGCTAAAATGAGAAATATCACCGAAATGAAAAA	1800						
Db	1741	GTAGAAAAGAGGAAGGAAATAATAATGCTAAAATGAGAAATATCACCGAAATGAAAAA	1800						
Qy	1801	ACTGATCGAAAATATACCGCTGCTAAAAGATACGGAAGGATGCTCTGCTAAGGTATA	1860						
Db	1801	ACTGATCGAAAATATACCGCTGCTAAAAGATACGGAAGGATGCTCTCTCTAAGGTATA	1860						
Qy	1861	TAACTGCTGGGAGAAAATGAAAACCTATATTTTAAAAATGACGACAGCCGTTATAAGG	1920						
Db	1861	TAACTGCTGGGAGAAAATGAAAACCTATATTTTAAAAATGACGACAGCCGTTATAAGG	1920						
Qy	1921	GACCACTATGATGGAACGGGAAAGGACATGATGCTATGGCTGGAAGGAAAGCTGCC	1980						
Db	1921	GACCACTATGATGGAACGGGAAAGGACATGATGCTATGGCTGGAAGGAAAGCTGCC	1980						
Qy	1981	TGTTCCAAAGGCTCGTCACTTTGTAACGGGCAATGAGTGGGCAATCTGCTCATGAGTGA	2040						
Db	1981	TGTTCCAAAGGCTCGTCACTTTGTAACGGGCAATGAGTGGGCAATCTGCTCATGAGTGA	2040						
Qy	2041	GGCGGATGGCGCTCTTGTGCTCGGAAGATATGAAGATGAACAAAGCCCTGAAAAGATTAT	2100						
Db	2041	GGCGGATGGCGCTCTTGTGCTCGGAAGATATGAAGATGAACAAAGCCCTGAAAAGATTAT	2100						
Qy	2101	CGAGCTGTATCGGAGTGCATCAGGCTTTTCTCACTCCATCGACATATCGGATTTGCCCTA	2160						

Db 2101 CGAGCTGATGCGGAGTGCATCAGGCTCTTTTCACTCCATCGACATATCGGATTTGCCCTA 2160  
Qy 2161 TAGCAATAGCTTAGACAGCGCTTAGCCGAATTGGATTACTTACTGAATAACGATCTGGC 2220  
Db 2161 TAGCAATAGCTTAGACAGCGCTTAGCCGAATTGGATTACTTACTGAATAACGATCTGGC 2220  
Qy 2221 CGATGTGGATTGGAAACCTGGGAAGAGACACTCCATTTAAAGATCCGCGGAGCTGTA 2280  
Db 2221 CGATGTGGATTGGAAACCTGGGAAGAGACACTCCATTTAAAGATCCGCGGAGCTGTA 2280  
Qy 2281 TGAATTTTAAAGACGAAAGCCGGAAGAGGACTTGTCTTTCCACGCGCACTGGG 2340  
Db 2281 TGAATTTTAAAGACGAAAGCCGGAAGAGGAACTTGTCTTTCCACGCGCACTGGG 2340  
Qy 2341 AGACAGCAACATCTTTGTGAAAGATGCAAAAGTAAGTGGCTTTATTGATCTTGGAGAAG 2400  
Db 2341 AGACAGCAACATCTTTGTGAAAGATGCAAAAGTAAGTGGCTTTATTGATCTTGGAGAAG 2400  
Qy 2401 CGGAGGCGGACAAAGTGGTATGACATTTGCTCTTCTCGCTCCGCTCGATCAGGAGGATAT 2460  
Db 2401 CGGAGGCGGACAAAGTGGTATGACATTTGCTCTTCTCGCTCCGCTCGATCAGGAGGATAT 2460  
Qy 2461 CGGGGAAGACAGTATGTCAGCTATTTTGTGACTTACTTGGGATCAAGCTGATTTGGGA 2520  
Db 2461 CGGGGAAGACAGTATGTCAGCTATTTTGTGACTTACTTGGGATCAAGCTGATTTGGGA 2520  
Qy 2521 GAAAAATAAATATATATTTTACTGGATGAATTTTGTAGTACTAGATGTGGCGAACG 2580  
Db 2521 GAAAAATAAATATATATTTTACTGGATGAATTTTGTAGTACTAGATGTGGCGAACG 2580  
Qy 2581 ATGCCGCGCAACAGCAGGAGCGCACCGACTTCTTCGCGATCAAGTGTTTTGGCTCTCAGG 2640  
Db 2581 ATGCCGCGCAACAGCAGGAGCGCACCGACTTCTTCGCGATCAAGTGTTTTGGCTCTCAGG 2640  
Qy 2641 CCGAGGCCACGGCAAGTATTTGGGCAAGGGTCTGCTGATTTCTGTCAGGGCAAGATTC 2700  
Db 2641 CCGAGGCCACGGCAAGTATTTGGGCAAGGGTCTGCTGATTTCTGTCAGGGCAAGATTC 2700  
Qy 2701 GGAATACCAAGTACGAGAAGACGGCCAGACGGTCTACGGGACCGACTTCATTTCGCGATA 2760  
Db 2701 GGAATACCAAGTACGAGAAGACGGCCAGACGGTCTACGGGACCGACTTCATTTCGCGATA 2760  
Qy 2761 AGGTGGATTATCTGGACCAACAGGCACAGGCGGGTCAAAATCAGGAATAAGGCACATTC 2820  
Db 2761 AGGTGGATTATCTGGACCAACAGGCACAGGCGGGTCAAAATCAGGAATAAGGCACATTC 2820  
Qy 2821 CCGCGGCTGAGTCGGGGCAATCCGCAAGGAGGTGAATGATCGGACGTTTGAACGGA 2880  
Db 2821 CCGCGGCTGAGTCGGGGCAATCCGCAAGGAGGTGAATGATCGGACGTTTGAACGGA 2880  
Qy 2881 AGGCATACGCAAGACTGATCGACGCGGGTTTTCCGCGGAGGATGCCGAACCATCG 2940  
Db 2881 AGGCATACGCAAGACTGATCGACGCGGGTTTTCCGCGGAGGATGCCGAACCATCG 2940  
Qy 2941 CAAGCCGACCGTCATCGTCGCGCCCGCGCAACCTTCCAGTCCGTCGGCTCGATGGTCC 3000  
Db 2941 CAAGCCGACCGTCATCGTCGCGCCCGCGCAACCTTCCAGTCCGTCGGCTCGATGGTCC 3000  
Qy 3001 AGCAAGCTACGGCCAGATCGAGGCGGACAGCTGCAACTTCCGCTCCGCTCCGCTCCGCG 3060  
Db 3001 AGCAAGCTACGGCCAGATCGAGGCGGACAGCTGCAACTTCCGCTCCGCTCCGCTCCGCG 3060  
Qy 3061 CGCCATCGCGCGCTGGAGCGTTTCGGTCTGTCGAAACAGGAGGCGGAGGTTTGGCGA 3120  
Db 3061 CGCCATCGCGCGCTGGAGCGTTTCGGTCTGTCGAAACAGGAGGCGGAGGTTTGGCGA 3120  
Qy 3121 AGTCGATGACCATCGACACCGGAGAACTATGACGACCAAGAAACCGCCGCGG 3180  
Db 3121 AGTCGATGACCATCGACACCGGAGAACTATGACGACCAAGAAACCGCCGCGG 3180  
Qy 3181 AGGACCTGGCAAAACAGGTACGAGGCCAAGCAGGCGCGTTCCTGAAACACACGAAGC 3240  
Db 3181 AGGACCTGGCAAAACAGGTACGAGGCCAAGCAGGCGCGTTCCTGAAACACACGAAGC 3240

Qy 3241 AGCAGATCAAGGAAATGCAGCTTTCTTGTTCGATATTGCGCGTGGCGGACACGATGC 3300  
Db 3241 AGCAGATCAAGGAAATGCAGCTTTCTTGTTCGATATTGCGCGTGGCGGACACGATGC 3300  
Qy 3301 GAGCGATGCGCAAAACGACAGCGCGCTCTGCGCTCTGCTTCCACACGCGCAACAAGAAATCC 3360  
Db 3301 GAGCGATGCGCAAAACGACAGCGCGCTCTGCGCTCTGCTTCCACACGCGCAACAAGAAATCC 3360  
Qy 3361 CGCGCAGGCGCTGCAAAAACAAGTTCATTTTCCACGCTCAACAGGACGTGAAGATCACCT 3420  
Db 3361 CGCGCAGGCGCTGCAAAAACAAGTTCATTTTCCACGCTCAACAGGACGTGAAGATCACCT 3420  
Qy 3421 ACACCGCGCTCGAGCTGCGGGCGGACGATGACGAACTGTGTGTGSGCAGAGTGTTCGAGT 3480  
Db 3421 ACACCGCGCTCGAGCTGCGGGCGGACGATGACGAACTGTGTGTGSGCAGAGTGTTCGAGT 3480  
Qy 3481 AGCGAAGCGCACCCCTATTCGGGGACCGATCACTTCACTGTTCTACGAGCTTTGCCAGG 3540  
Db 3481 AGCGAAGCGCACCCCTATTCGGGGACCGATCACTTCACTGTTCTACGAGCTTTGCCAGG 3540  
Qy 3541 ACCTGGCTGGTCGATCAATGCGCGCTATTACACGAAGCCGAGGAATGCCTCTCGCGCC 3600  
Db 3541 ACCTGGCTGGTCGATCAATGCGCGCTATTACACGAAGCCGAGGAATGCCTCTCGCGCC 3600  
Qy 3601 TACAGCGCAGCGCGATGGGCTTCACTCCGACCGCGTTGGGCACTTGGAAATCGGTGTGCG 3660  
Db 3601 TACAGCGCAGCGCGATGGGCTTCACTCCGACCGCGTTGGGCACTTGGAAATCGGTGTGCG 3660  
Qy 3661 TGTGCAACCGCTTCCGCTCTGGAACCGTGGCAAGAAACGTCCTGTCAGGTCTGTA 3720  
Db 3661 TGTGCAACCGCTTCCGCTCTGGAACCGTGGCAAGAAACGTCCTGTCAGGTCTGTA 3720  
Qy 3721 TCGACAGGAAATCGTCTGCTTTTGTGGGACCACTACACGAATTCATATGGGAGA 3780  
Db 3721 TCGACAGGAAATCGTCTGCTTTTGTGGGACCACTACACGAATTCATATGGGAGA 3780  
Qy 3781 AGTACCGCAAGCTGTCCGCGCGGCGGACCGAGTGTTCGACTATTTTCAGCTCCGACCGGG 3840  
Db 3781 AGTACCGCAAGCTGTCCGCGCGGCGGACCGAGTGTTCGACTATTTTCAGCTCCGACCGGG 3840  
Qy 3841 AGCGGTACCGCTCAAGCTTGGAAAACTTCCGCTCATGTGCGGATCGGATTTCCACCGCG 3900  
Db 3841 AGCGGTACCGCTCAAGCTTGGAAAACTTCCGCTCATGTGCGGATCGGATTTCCACCGCG 3900  
Qy 3901 TGAAGAGTGGCGGAGCAGGTCCGGAAGCTTGGCAAGAGTTGCGAGGCGCGGCTGG 3960  
Db 3901 TGAAGAGTGGCGGAGCAGGTCCGGAAGCTTGGCAAGAGTTGCGAGGCGCGGCTGG 3960  
Qy 3961 TGGAAACACGCTGGGTCAATGATGACCTGCTGATTTGCAAAACGCTAGGGCTTTGTGGGT 4020  
Db 3961 TGGAAACACGCTGGGTCAATGATGACCTGCTGATTTGCAAAACGCTAGGGCTTTGTGGGT 4020  
Qy 4021 CAGTCCGCTGGGGTTTTCAGCAGCAGCGCTTTACTGCAATTTTCAGGTTCAGCTTT 4080  
Db 4021 CAGTCCGCTGGGGTTTTCAGCAGCAGCGCTTTACTGCAATTTTCAGGTTCAGCTTT 4080  
Qy 4081 CTGATGGGCTGCTGATCGAGTGGTGAATTTGTCGCGGAGCTCCGCTCGGGAGCTGTT 4140  
Db 4081 CTGATGGGCTGCTGATCGAGTGGTGAATTTGTCGCGGAGCTCCGCTCGGGAGCTGTT 4140  
Qy 4141 GGTGGCTGGTGGCAGGATATTTGCTGTGTAACAAATTTGACGCTTAGACAACTTAATA 4200  
Db 4141 GGTGGCTGGTGGCAGGATATTTGCTGTGTAACAAATTTGACGCTTAGACAACTTAATA 4200  
Qy 4201 ACACATTCGGAGCTTTTAAATGTAAGTGGGCTATCCCGGGGGATATCCATAGGCCG 4260  
Db 4201 ACACATTCGGAGCTTTTAAATGTAAGTGGGCTATCCCGGGGGATATCCATAGGCCG 4260  
Qy 4261 ATCTAGTAACATAATGACACCGCGCGGATATTTATCTAGTTTTCGCGCTATATTTTG 4320  
Db 4261 ATCTAGTAACATAATGACACCGCGCGGATATTTATCTAGTTTTCGCGCTATATTTTG 4320







Qy	601	CTTCTCGAACCTCCGGAAGGTATGCGGTGTAATAACCGCACAGATCGGTAAAGAGA	660
Db	601	CTTCTCGAACCTCCGGAAGGTATGCGGTGTAATAACCGCACAGATCGGTAAAGAGA	660
Qy	661	AAATACCGCATCAGCGCTCTTCGCTTCCTCGCTCACTGACTCGCTCGCTCGGTGCTT	720
Db	661	AAATACCGCATCAGCGCTCTTCGCTTCCTCGCTCACTGACTCGCTCGGTGCTT	720
Qy	721	CGGCTGGCGGAGCGGTATCAGCTCACTCAAAGCGGTAAATACGGTTATCCACAGAAATCA	780
Db	721	CGGCTGGCGGAGCGGTATCAGCTCACTCAAAGCGGTAAATACGGTTATCCACAGAAATCA	780
Qy	781	GGGGTAACCGCAGGAAGACATGTGAGCAAAAGGCCAGAAAAGGCCAGGAACCGTAAA	840
Db	781	GGGGTAACCGCAGGAAGACATGTGAGCAAAAGGCCAGAAAAGGCCAGGAACCGTAAA	840
Qy	841	AAGGCCGGTGTCTGGGCTTTTCCATAGGCTCGCGCCCTGACGAGCATCAAAAAAT	900
Db	841	AAGGCCGGTGTCTGGGCTTTTCCATAGGCTCGCGCCCTGACGAGCATCAAAAAAT	900
Qy	901	CGACGCTCAAGTCAGAGGTGGCAAAACCCGACAGGACTATAAAGATACCAAGGCGTTCCC	960
Db	901	CGACGCTCAAGTCAGAGGTGGCAAAACCCGACAGGACTATAAAGATACCAAGGCGTTCCC	960
Qy	961	CCTGGAGCTCCTCGTGGCTCTCTGTTCCGACCCCTGCGGCTTACCGGATACCTGTCC	1020
Db	961	CCTGGAGCTCCTCGTGGCTCTCTGTTCCGACCCCTGCGGCTTACCGGATACCTGTCC	1020
Qy	1021	GCCTTCTCCCTCGGAAGCGTGGCGCTTCTCATAGCTCACGCTGAGGTATCTCAGT	1080
Db	1021	GCCTTCTCCCTCGGAAGCGTGGCGCTTCTCATAGCTCACGCTGAGGTATCTCAGT	1080
Qy	1081	TCGGTGTAGTTCGTTTCGCTCCAAAGCTGGGCTGTGTGCACGAACCCCGCTTCAGCCCGAC	1140
Db	1081	TCGGTGTAGTTCGTTTCGCTCCAAAGCTGGGCTGTGTGCACGAACCCCGCTTCAGCCCGAC	1140
Qy	1141	CGCTGGCGCTTATCCGGTAACTATCGTCTTGAGTCCAAACCGGTAAACACGACTTATCG	1200
Db	1141	CGCTGGCGCTTATCCGGTAACTATCGTCTTGAGTCCAAACCGGTAAACACGACTTATCG	1200
Qy	1201	CCACTGGCAGCGCTTCTACCAATAACCGGATAAACCCAGCGAACATTCAGGTGAT	1260
Db	1201	CCACTGGCAGCGCTTCTACCAATAACCGGATAAACCCAGCGAACATTCAGGTGAT	1260
Qy	1261	AGGTAAGATTATACCGAGGTATGAAAACGAGAATTGGACCTTTACAGAAATCTCTATGA	1320
Db	1261	AGGTAAGATTATACCGAGGTATGAAAACGAGAATTGGACCTTTACAGAAATCTCTATGA	1320
Qy	1321	AGGCCCATATTTAAAAAGCTACCAAGACGAAGGATGAAGAGATGAGGAGCGAGATTG	1380
Db	1321	AGGCCCATATTTAAAAAGCTACCAAGACGAAGGATGAAGAGATGAGGAGCGAGATTG	1380
Qy	1381	CTTTGAATATATTACAACTACTGATAGATAATACATCTTTTATATAGAAGATATCGCG	1440
Db	1381	CTTTGAATATATTACAACTACTGATAGATAATACATCTTTTATATAGAAGATATCGCG	1440
Qy	1441	TATGTAAGGATTTTCAAGGGGCAAGGCATAGCAGCGGCTTATCAATATATCTATAGAAT	1500
Db	1441	TATGTAAGGATTTTCAAGGGGCAAGGCATAGCAGCGGCTTATCAATATATCTATAGAAT	1500
Qy	1501	GGGCAAGCATAAAACTTGATGAAAGCTGTTTCTCGTATTTAAAGTTTTAGAAATGCAA	1560
Db	1501	GGGCAAGCATAAAACTTGATGAAAGCTGTTTCTCGTATTTAAAGTTTTAGAAATGCAA	1560
Qy	1561	CTTGTAAATTTTACCAAAATTTGGTTTCAAAATCGGCTCGGTGATCTATGTTATACG	1620
Db	1561	CTTGTAAATTTTACCAAAATTTGGTTTCAAAATCGGCTCGGTGATCTATGTTATACG	1620
Qy	1621	CCAACTTTGAAAACAACTTTGAAAAGCTGTTTCTCGTATTTAAAGTTTTAGAAATGCAA	1680
Db	1621	CCAACTTTGAAAACAACTTTGAAAAGCTGTTTCTCGTATTTAAAGTTTTAGAAATGCAA	1680
Qy	1681	GGAAACAGTGAATTGGAGTTGCTCTGTTTAAATTAGCTTCTTGGGGTATCTTTAAATFAC	1740

Db	1681		GGAACAGTGAATGGGAGTTGCTTGTATTATAATTAAGCTTCTGGGGTATCTTTAAATACT	1740
Qy	1741		GTAGAAAAGAGGAAGGAAATAATAATGGCTAAAAATGAGAATATCACCGGAATTTGAAAAA	1800
Db	1741		GTAGAAAAGAGGNAAGGAATATAAATGGCTAAATGAGAATATCACCGGAATTTGAAAAA	1800
Qy	1801		ACTGATCGAAAAATACCGCTGCGTAAAAAGATACGGAAGAAATGTCTCTGCTGATAGGTATA	1860
Db	1801		ACTGATCGAAAAATACCGCTGCGTAAAAAGATACGGAAGAAATGTCTCTGCTGATAGGTATA	1860
Qy	1861		TAAAGCTGGTGGGAGAAAATGAAAACCTATATTAAARAATGACGGACAGCCGGTATAAAGG	1920
Db	1861		TAAAGCTGGTGGGAGAAAATGAAAACCTATATTAAARAATGACGGACAGCCGGTATAAAGG	1920
Qy	1921		GACCACTATGATGTGGAAACGGAAAAAGACATGATGCTATGGCTGGAAGGAAAAGCTGCC	1980
Db	1921		GACCACTATGATGTGGAAACGGAAAAAGACATGATGCTATGGCTGGAAGGAAAAGCTGCC	1980
Qy	1981		TGTTCCAAAGGCTCTGCACATTTTGAACGGCATGATGGCTGGAGCAATCTGCTCATGAGTGA	2040
Db	1981		TGTTCCAAAGGCTCTGCACATTTTGAACGGCATGATGGCTGGAGCAATCTGCTCATGAGTGA	2040
Qy	2041		GGCCGATGGCTCCTTTGCTCGGAAGAGTATGAAGATGAACAAAGCCCTGGAAGAATAT	2100
Db	2041		GGCCGATGGCTCCTTTGCTCGGAAGAGTATGAAGATGAACAAAGCCCTGGAAGAATAT	2100
Qy	2101		CGAGCTGTATGCGGAGTGATCAGAGCTCTTTCACTCCATCGACATATCGGAATTTGCCCTA	2160
Db	2101		CGAGCTGTATGCGGAGTGATCAGAGCTCTTTCACTCCATCGACATATCGGAATTTGCCCTA	2160
Qy	2161		TACGAATAGCTTTAGACAGCCGCTTAGCCGAATTTGATTTACTTGAATAACGATCTGGC	2220
Db	2161		TACGAATAGCTTTAGACAGCCGCTTAGCCGAATTTGATTTACTTGAATAACGATCTGGC	2220
Qy	2221		CGATGTGGATTCGGAATACTGGGAAGAAGACATCTCCATTTAAAGATCCGCGGAGCTGTA	2280
Db	2221		CGATGTGGATTCGGAATACTGGGAAGAAGACATCTCCATTTAAAGATCCGCGGAGCTGTA	2280
Qy	2281		TGATTTTTTAAAGACGGAAGAACCCCGAAGAGGAACCTGCTCTTTTCCACGCGACCTGGG	2340
Db	2281		TGATTTTTTAAAGACGGAAGAACCCCGAAGAGGAACCTGCTCTTTTCCACGCGACCTGGG	2340
Qy	2341		AGACAGCAACATCTTTGTGAAAGATGGCAAAAGTAAAGTGGCTTTATTTGATCTTTGGGAGAAG	2400
Db	2341		AGACAGCAACATCTTTGTGAAAGATGGCAAAAGTAAAGTGGCTTTATTTGATCTTTGGGAGAAG	2400
Qy	2401		CGGCGGGCGGACAAGTGGTATGACAATTGCCCTTCGCTCGGTCGATCAGGGAGGATAT	2460
Db	2401		CGGCGGGCGGACAAGTGGTATGACAATTGCCCTTCGCTCGGTCGATCAGGGAGGATAT	2460
Qy	2461		CGGGGAAGAACAGTATGTCAGACTATTTTTCACCTTACTGGGGATCAAGCCTGATGGGA	2520
Db	2461		CGGGGAAGAACAGTATGTCAGACTATTTTTCACCTTACTGGGGATCAAGCCTGATGGGA	2520
Qy	2521		GAAATAAAAATATATATTTTACTGGATGAATTTGTTTGTAGTACCTAGATGTGGCGCAACG	2580
Db	2521		GAAATAAAAATATATATTTTACTGGATGAATTTGTTTGTAGTACCTAGATGTGGCGCAACG	2580
Qy	2581		ATGCGGGCGACAAAGCAGGAGCGCACCGATTCCTCCGATCAAGTGTTTTGGCTCTCAGG	2640
Db	2581		ATGCGGGCGACAAAGCAGGAGCGCACCGATTCCTCCGATCAAGTGTTTTGGCTCTCAGG	2640
Qy	2641		CCGAGGCCCAACGGCAAGTATTTGGCAAGGGGTGCTGGTATTCGTCAGGGCGCAAGATTC	2700
Db	2641		CCGAGGCCCAACGGCAAGTATTTGGCAAGGGGTGCTGGTATTCGTCAGGGCGCAAGATTC	2700
Qy	2701		GGAATACCAAGTACGAGAAGGACGCCAGACGGTCTACGGACCGCATCTCATTTGCCGATA	2760
Db	2701		GGAATACCAAGTACGAGAAGGACGCCAGACGGTCTACGGACCGCATCTCATTTGCCGATA	2760
Qy	2761		AGTGTGATTTATCTGGACACCAAGGCAACGCGGGTCAAATCAGGAATTAAGGGCACATTTG	2820

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Db 2761 AGGTGGATTATCTGGACACCAAGGCACAGGCGGGTCAAAATCAGGAATTAAGGGACATTG 2820
Qy 2821 CCCGGCGTGAGTCGGGGCAATCCCGCAAGAGGGTGAATGAATCGAAGCTTTGACCCGGA 2880
Db 2821 CCCGGCGTGAGTCGGGGCAATCCCGCAAGAGGGTGAATGAATCGAAGCTTTGACCCGGA 2880
Qy 2881 AGGCATACAGGCAAGAACTCATCGACCGGGGTTTTCCGCGGAGGATGCCGAAACCATCG 2940
Db 2881 AGGCATACAGGCAAGAACTCATCGACCGGGGTTTTCCGCGGAGGATGCCGAAACCATCG 2940
Qy 2941 CAAGCCGACCGTCATCCGTGCGGCCCGCGCAAACTTCCAGTCCGTCGGCTCGATGCTCC 3000
Db 2941 CAAGCCGACCGTCATCCGTGCGGCCCGCGCAAACTTCCAGTCCGTCGGCTCGATGCTCC 3000
Qy 3001 AGCAAGCTACGGCCAAAGATCGAGCGCGACAGCGTGCAACTGGGTCCCTCGCCCTGCCCG 3060
Db 3001 AGCAAGCTACGGCCAAAGATCGAGCGCGACAGCGTGCAACTGGGTCCCTCGCCCTGCCCG 3060
Qy 3061 CGCCATCGGCGCGCGTGGAGCGTTTCGGTCTGCTCTCGAAACAGGAGCGGAGGTTTGGCGA 3120
Db 3061 CGCCATCGGCGCGCGTGGAGCGTTTCGGTCTGCTCTCGAAACAGGAGCGGAGGTTTGGCGA 3120
Qy 3121 AGTCGATGACCATCGACACGCGAGGAACTATGACGACCAAGAGCGGAAACCGCCCGCG 3180
Db 3121 AGTCGATGACCATCGACACGCGAGGAACTATGACGACCAAGAGCGGAAACCGCCCGCG 3180
Qy 3181 AGGACCTGGCAAAACAGGTCAGCGGCGCAAGAGCCGCGTTGCTGAAACACACGAAAGC 3240
Db 3181 AGGACCTGGCAAAACAGGTCAGCGGCGCAAGAGCCGCGTTGCTGAAACACACGAAAGC 3240
Qy 3241 AGCAGATCAAGGAATCGAGCTTTCTTGTTCGATATTCGCGCGTGGCGGACACGATGC 3300
Db 3241 AGCAGATCAAGGAATCGAGCTTTCTTGTTCGATATTCGCGCGTGGCGGACACGATGC 3300
Qy 3301 GAGCGATGCCAAACGACACGCGCCGCTCTGCGCTGTTTCAACACGCGCAACAGAAATCC 3360
Db 3301 GAGCGATGCCAAACGACACGCGCCGCTCTGCGCTGTTTCAACACGCGCAACAGAAATCC 3360
Qy 3361 CGCGCGAGGCGTCAAAAACAGGTCAATTTTCCACGTCAACAGGAGCGTGAAGATCACCT 3420
Db 3361 CGCGCGAGGCGTCAAAAACAGGTCAATTTTCCACGTCAACAGGAGCGTGAAGATCACCT 3420
Qy 3421 ACACCGCGTCGAGCTCGGGCGGACGATGACGAACTGGTGTGCGACGAGGTGTTGAGT 3480
Db 3421 ACACCGCGTCGAGCTCGGGCGGACGATGACGAACTGGTGTGCGACGAGGTGTTGAGT 3480
Qy 3481 ACGCGAAGCGCACCCCTATCGGCGAGCGGATCACTTTCAGCTTCTACGAGCTTTGCCAGG 3540
Db 3481 ACGCGAAGCGCACCCCTATCGGCGAGCGGATCACTTTCAGCTTCTACGAGCTTTGCCAGG 3540
Qy 3541 ACCTGGGCTGGTCAATGGCCGGTATTACAGAAAGGCGGAGGAATGCCCTGTCGGGCC 3600
Db 3541 ACCTGGGCTGGTCAATGGCCGGTATTACAGAAAGGCGGAGGAATGCCCTGTCGGGCC 3600
Qy 3601 TACAGGCGACGGCATGGGCTTACGTCGACCGCGTGGGACCTTGGGACCTGCGTGTGCG 3660
Db 3601 TACAGGCGACGGCATGGGCTTACGTCGACCGCGTGGGACCTTGGGACCTGCGTGTGCG 3660
Qy 3661 TGCTGCAACCGCTTCGGGCTCTGGACCGTGGCAAGAAACGTTCCCGTTGCCAGTCTCTGA 3720
Db 3661 TGCTGCAACCGCTTCGGGCTCTGGACCGTGGCAAGAAACGTTCCCGTTGCCAGTCTCTGA 3720
Qy 3721 TCAGCAGGGAATCGTCTGCTGTTTGTGTCGCGACCACTACACGAAATTCATATGGGAGA 3780
Db 3721 TCAGCAGGGAATCGTCTGCTGTTTGTGTCGCGACCACTACACGAAATTCATATGGGAGA 3780
Qy 3781 AGTACCGCAAGCTTCTGCCGACGCGCGCGAGGATGTTTCGACTATTTTCACTCGCACCGGG 3840
Db 3781 AGTACCGCAAGCTTCTGCCGACGCGCGCGAGGATGTTTCGACTATTTTCACTCGCACCGGG 3840
Qy 3841 AGCGGTACCCGCTCAAGCTGGAACCTTCCGCTCATGTGGGGATCGGATTTCCACCCGCG 3900
Db 3841 AGCGGTACCCGCTCAAGCTGGAACCTTCCGCTCATGTGGGGATCGGATTTCCACCCGCG 3900
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Qy 3901 TGAAGAAGTGGCGCAGCAGGTCGGGAAGCCTTGCAGAGTTTGCAGGCGAGCGGCTGG 3960
Db 3901 TGAAGAAGTGGCGCAGCAGGTCGGGAAGCCTTGCAGAGTTTGCAGGCGAGCGGCTGG 3960
Qy 3961 TGAACAACAGCCTGGGTCATATGATGACCTGGTGCATTGCAAAACGCTAGGCGCTTGTGGGT 4020
Db 3961 TGAACAACAGCCTGGGTCATATGATGACCTGGTGCATTGCAAAACGCTAGGCGCTTGTGGGT 4020
Qy 4021 CAGTTCGGGCTGGGGTTTCAGCAGCCAGCGCTTTTACTGSCATTTCTAGTTGACCTCTT 4080
Db 4021 CAGTTCGGGCTGGGGTTTCAGCAGCCAGCGCTTTTACTGSCATTTCTAGTTGACCTCTT 4080
Qy 4081 CTGATCGGCTGCCGTGATCGAGTGGTGATTTTGTGCGAGCTGCCGCTCGGGAGCTGTT 4140
Db 4081 CTGATCGGCTGCCGTGATCGAGTGGTGATTTTGTGCGAGCTGCCGCTCGGGAGCTGTT 4140
Qy 4141 GGCTGGCTGGTGGCAGGATATATTTGTTGTTAAACAAATTTGACGCTTAGACAACTTAATA 4200
Db 4141 GGCTGGCTGGTGGCAGGATATATTTGTTGTTAAACAAATTTGACGCTTAGACAACTTAATA 4200
Qy 4201 ACACATTTGGGAGCTTTTAAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATG 4260
Db 4201 ACACATTTGGGAGCTTTTAAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATG 4260
Qy 4261 ATCTAGTAAACATAATCACACCGCGCGGATATTTATCTAGTTTTCGCGCTATATTTTG 4320
Db 4261 ATCTAGTAAACATAATCACACCGCGCGGATATTTATCTAGTTTTCGCGCTATATTTTG 4320
Qy 4321 TTTTCTATCGCGTATTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATG 4380
Db 4321 TTTTCTATCGCGTATTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATG 4380
Qy 4381 AATAACGTCATGCAATTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATG 4440
Db 4381 AATAACGTCATGCAATTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATG 4440
Qy 4441 ATGATTAATCATCGCAAGACCGCAACAGGATTCATCTTAAGAACTTTTATTCGCAAAATG 4500
Db 4441 ATGATTAATCATCGCAAGACCGCAACAGGATTCATCTTAAGAACTTTTATTCGCAAAATG 4500
Qy 4501 TTTGAAACGATCGTTTCGTCGAGCTATGGGCCGA 4533
Db 4501 TTTGAAACGATCGTTTCGTCGAGCTATGGGCCGA 4533
```

## RESULT 14

AAF80288  
ID AAF80288 standard; DNA; 8654 BP.

XX AAF80288;

XX 29-JUN-2001 (first entry)

XX Nucleotide sequence of plasmid pMRT1196.

XX Vector; transgenesis; trfA locus; RK2 ori; oriV; P285 protein;  
XX P382 protein; antibiotic resistance gene; nptIII; transgenic plant; ss.

XX Synthetic.

Key	Location/Qualifiers
rep_origin	1..654
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	/note= "ori RK2"
rep_origin	655..1263
	/*tag= b
	/note= "ori Cole1"
CDS	1264..2603
	/*tag= c
	/note= "NPT III gene coding for neomycin phosphotransferase and kanamycin resistance"
CDS	2604..4098

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FT /*tag= d
FT /note= "trfA locus from RK2 coding for two proteins P285
FT and P382 enabling an increase in the replication rate"
FT misc_feature 4106..4271
FT /*tag= e
FT /note= "T-DNA left border"
FT terminator 4272..4559
FT /*tag= f
FT /note= "nopaline synthetase terminator"
FT CDS 4560..5556
FT /*tag= g
FT /note= "NPT III gene coding for neomycin
FT phosphotransferase and kanamycin resistance"
FT promoter 5557..5771
FT /*tag= h
FT /note= "nopaline synthetase promoter"
FT CDS 5818..7717
FT /*tag= i
FT /note= "GUS gene coding for beta glucuronidase"
FT polyA_signal 7718..8447
FT /*tag= j
FT /note= "polyA from 35S ribosome"
FT misc_feature 8474..8647
FT /*tag= k
FT /note= "T-DNA right border"
FT FT
XX PR2798139-A1.
XX
XX
XX 09-MAR-2001.
XX
XX 03-SEP-1999; 99FR-00011112.
XX
XX 03-SEP-1999; 99FR-00011112.
XX
XX (MERI-) MERISTEM THERAPEUTICS SA.
XX
XX Gruber V, Comeau D;
XX WPI; 2001-259847/27.
XX
XX New vector free from non-essential elements, useful for transforming
XX cells for protein production and for preparing transgenic plants.
XX
XX Claim 20; Page 132-135; 180pp; French.
XX
XX The specification describes a synthetic vector containing only those
XX elements essential for its functionality and transgenesis of a cell
XX (especially a plant cell). The vector consists of at most one origin of
XX replication (ori), at most one sequence encoding a selection agent and a
XX trfA locus encoding a protein that increases the level of plasmid
XX replication. The vector particularly contains an RK2 ori, especially oriV
XX from PRK2 of Escherichia coli with a broad host range, an antibiotic
XX resistance gene (especially nptII conferring resistance to kanamycin in
XX bacteria) and a trfA locus from PRK2 encoding the proteins P285 and P382.
XX The vectors are used to prepare transgenic plants and transformed host
XX cells for production of a heterologous proteins, e.g. insulin,
XX interferon, lipase, blood proteins and anti-inflammatory agents. The
XX present sequence represents a plasmid of the invention
XX
XX Sequence 8654 BP; 2243 A; 2134 C; 2352 G; 1925 T; 0 U; 0 Other;
XX
XX Query Match 94.3%; Score 4531.4; DB 4; Length 8654;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 4532; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1 CCGGGCTGGTTCCTCGCGCTGGGCTGGCGCGCTATGCGCTGCAAAACGCCCCAG 60
XX |
XX 1 CCGGGCTGGTTCCTCGCGCTGGGCTGGCGCGCTATGCGCTGCAAAACGCCCCAG 60
XX |
XX 61 AAACGCCGTCGAACCGGTGTGCAGACACCGCGCGCGCGGCTGTGTGATACCTCGGG 120
XX |
XX 61 AAACGCCGTCGAACCGGTGTGTGAGTAACTATGCTCTTGTGAGTCCAAACGCCGCTTATCG 1200
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XX 1201 CCACTGGCAGCAGCCTTCTACCATTAATCCGCGATAAACCCAGCAACCATTTGAGGTGAT 1260
XX |
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QY 121 AAAAATTGGCCCTCACTGACAGATGAGGGCGGACGCTTGACACTTGAGGGCGGACTCAC 180
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DB 121 AAAAATTGGCCCTCACTGACAGATGAGGGCGGACGCTTGACACTTGAGGGCGGACTCAC 180
QY 181 CCGGCGCGGCTTGACAGATGAGGGCGGAGCTCGATTTCCGCGCGGACGCTGAGCTGGC 240
DB |
DB 181 CCGGCGCGGCTTGACAGATGAGGGCGGAGCTCGATTTCCGCGCGGACGCTGAGCTGGC 240
QY 241 CAGCCTCGCAAAATCGGCGAAACCGCTGATTTTACGCGAGTTTCCACACAGATGATGGGA 300
DB |
DB 241 CAGCCTCGCAAAATCGGCGAAACCGCTGATTTTACGCGAGTTTCCACACAGATGATGGGA 300
QY 301 CAAAGCTTGGGGATTAAGTGGCCCTGCGGTATTTGACACTTGAGGGCGGAGCTACTGACAGAT 360
DB |
DB 301 CAAAGCTTGGGGATTAAGTGGCCCTGCGGTATTTGACACTTGAGGGCGGAGCTACTGACAGAT 360
QY 361 GAGGGCGGAGTCTTTGACACTTTGAGGGCGGAGTCTGACAGATGAGGGCGGAGCTAT 420
DB |
DB 361 GAGGGCGGAGTCTTTGACACTTTGAGGGCGGAGTCTGACAGATGAGGGCGGAGCTAT 420
QY 421 TGACATTTGAGGGCTGTCCACAGGCGAGAAATCCAGCATTTTCAAGGGTTTCCGCCCGT 480
DB |
DB 421 TGACATTTGAGGGCTGTCCACAGGCGAGAAATCCAGCATTTTCAAGGGTTTCCGCCCGT 480
QY 481 TTTTCGGCCACCGCTAACCTGTCTTTTAACTGCTTTTAAACCAATATTTATAAACCCTTG 540
DB |
DB 481 TTTTCGGCCACCGCTAACCTGTCTTTTAACTGCTTTTAAACCAATATTTATAAACCCTTG 540
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DB |
DB 541 TTTTAAACAGGGCTGGCCCTGTGCGCGTGACCGCGCAGCGCGAAGGGGGTTCGCCCCC 600
QY 601 CTTTCTCGAAACCTCCCGGAAAGGTATGCGGTGTGAAATACCGCACAGATCGTAAGGAGA 660
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DB 601 CTTTCTCGAAACCTCCCGGAAAGGTATGCGGTGTGAAATACCGCACAGATCGTAAGGAGA 660
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DB |
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DB 721 CGGCTCGGGGAGCGGTATCAGCTCACTCAAGGGCGGTAAATACGGTTATCCACAGATCA 780
QY 781 GGGGATAACCGAGGAAAGACATGTGAGCAAAAGGCGCAAAAGGCCAGGAACCGTAAA 840
DB |
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DB 841 AAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCGCTGACGAGCATCAAAAAAT 900
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DB 1141 CGCTGGCCTTATCCGGTAACCTATCGTCTTGTAGTCCAAACCCCGTAAAGACGACTTATCG 1200
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DB |
```



```
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Db 3421 ACACCGCGTCGAGCTCGCGGCCGACGATACGAACCTGGTGTGGCAGCAGGTGTGGAGT 3480
QY 3481 ACCGAGCGCACCCCTATCGCGAGCGGATCACTTCAGTTCCTACGAGCTTTGCCAGG 3540
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QY 3661 TGGTGCACCGCTTCGCGCTCTCGACCGTGGGAGAAAGTCCCGTGGCAGGCTCTGA 3720
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QY 4381 AATAAGCTCATGATTAATGATTAATTAATGATTAATTAATGATTAATTAATGATTAAT 4440
Db 4381 AATAAGCTCATGATTAATGATTAATTAATGATTAATTAATGATTAATTAATGATTAAT 4440
QY 4441 ATGATAATCATCGCAGACCGGCAACAGGATTCATCTTAAGAACTTTATTCGCAATG 4500
Db 4441 ATGATAATCATCGCAGACCGGCAACAGGATTCATCTTAAGAACTTTATTCGCAATG 4500
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QY 4501 TTTGAACGATCGTTCGTCGAGCTATGGGCCGA 4533
Db 4501 TTTGAACGATCGTTCGTCGAGCTATGGGCCGA 4533

RESULT 15
AAF80296
ID AAF80296 standard; DNA; 8987 BP.
XX
AC AAF80296;
XX
DT 29-JUN-2001 (first entry)
XX
Nucleotide sequence of plasmid pMRT1212.
DE
XX
Vector; transgenesis; trfA locus; RK2 ori; oriV; P285 protein;
KW P382 protein; antibiotic resistance gene; nptIII; transgenic plant; ss.
XX
OS Synthetic.
XX
Key Location/Qualifiers
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FT /tag= a
FT /note= "ori RK2"
FT rep_origin 655..1263
FT /tag= b
FT /note= "ori ColE1"
FT CDS 1264..2603
FT /tag= c
FT /note= "NPT III gene coding for neomycin
FT phosphotransferase and kanamycin resistance"
FT CDS 2604..4098
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FT /note= "TrfA locus from RK2 coding for two proteins P285
FT and P382 enabling an increase in the replication rate"
FT terminator 4272..4559
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FT CDS 4575..5150
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FT /note= "Bar gene coding for phosphinotricin
FT acetyltransferase and glufosinate resistance"
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FT promoter 5369..6111
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FT CDS 6159..8050
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FR2798139-A1.
XX
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XX
PF 03-SEP-1999; 99FR-00011112.
XX
PR 03-SEP-1999; 99FR-00011112.
XX (MERI-) MERISTEM THERAPEUTICS SA.
XX Gruber V, Comeau D;
XX WPI; 2001-259847/27.
XX New vector free from non-essential elements, useful for transforming
PT
```

cells for protein production and for preparing transgenic plants.

Claim 20; Page 168-171; 180pp; French.

The specification describes a synthetic vector containing only those elements essential for its functionality and transgenesis of a cell (especially a plant cell). The vector consists of at most one origin of replication (ori), at most one sequence encoding a selection agent and a trfA locus encoding a protein that increases the level of plasmid replication. The vector particularly contains an RK2 ori, especially oriV from pRK2 of *Escherichia coli* with a broad host range, an antibiotic resistance gene (especially nptIII conferring resistance to kanamycin in bacteria) and a trfA locus from pRK2 encoding the proteins P285 and P382. The vectors are used to prepare transgenic plants and transformed host cells for production of a heterologous proteins, e.g. insulin, interferon, lipase, blood proteins and anti-inflammatory agents. The present sequence represents a plasmid of the invention

Sequence 8987 BP; 2342 A; 2205 C; 2438 G; 2002 T; 0 U; 0 Other;

very Match 94.3%; Score 4531.4; DB 4; Length 8987;

1st Local Similarity 100.0%; Pred. No. 0;

Matches 4532; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1	CGGGCTGGTTCGCTCGCGCTGGGCTGGCGGCGGTCTATGGCCCTCGAAACGGCCAG	60
1	CGGGCTGGTTCGCTCGCGCTGGGCTGGCGGCGGTCTATGGCCCTCGAAACGGCCAG	60
61	AAACGCGGTCGAAGCCGTGTGCGACACACCGCGGCGCGCGGCTTGTGGATCTACCTCGGG	120
61	AAACGCGGTCGAAGCCGTGTGCGACACACCGCGGCGCGCGGCTTGTGGATCTACCTCGGG	120
121	AAAACTTGGCCCTCACTGACAGATGAGGGCGGACGTTTGACACTTTGAGGGCGGACTCAC	180
121	AAAACTTGGCCCTCACTGACAGATGAGGGCGGACGTTTGACACTTTGAGGGCGGACTCAC	180
181	CGGGCGGCGGTTGACAGATGAGGGCGAGGCTCGATTTGCGCGCGCGACGTGGAGCTGGC	240
181	CGGGCGGCGGTTGACAGATGAGGGCGAGGCTCGATTTGCGCGCGCGACGTGGAGCTGGC	240
241	CAGCCTCGCAATCGCGGAAACGGCTGATTTATCGCGAGTTTCCACACAGATGATGTGGA	300
241	CAGCCTCGCAATCGCGGAAACGGCTGATTTATCGCGAGTTTCCACACAGATGATGTGGA	300
301	CAAGCTCGGGGATAGTGCCTCGGCTATTGACACTTTGAGGGCGCGACTACTGCACAGAT	360
301	CAAGCTCGGGGATAGTGCCTCGGCTATTGACACTTTGAGGGCGCGACTACTGCACAGAT	360
361	GAGGGCGCGATCTTTGACACTTTGAGGGCGACAGTGTCTGACAGATGAGGGGCGCACCTAT	420
361	GAGGGCGCGATCTTTGACACTTTGAGGGCGACAGTGTCTGACAGATGAGGGGCGCACCTAT	420
421	TGACATTTGAGGGGCTGTCCACAGGCAGAAAAATTCAGACATTTTGCAAGGGTTTCGCCCGGT	480
421	TGACATTTGAGGGGCTGTCCACAGGCAGAAAAATTCAGACATTTTGCAAGGGTTTCGCCCGGT	480
481	TTTTTCGCCCAACCGCTAACTGTCTTTTAACTGCTTTTAAACCAATATTTATAAACCTTG	540
481	TTTTTCGCCCAACCGCTAACTGTCTTTTAACTGCTTTTAAACCAATATTTATAAACCTTG	540
541	TTTTTTAAACAGGGCTCGGCCCTGTGCGCGTGACCGCGCACCGGAGGGGGTGCCCGCC	600
541	TTTTTTAAACAGGGCTCGGCCCTGTGCGCGTGACCGCGCACCGGAGGGGGTGCCCGCC	600
601	CTTCTCGAAACCTTCCCGGAAAGGTATGCGGTGTGAAATACCGCACAGATGCGTAAAGGAGA	660
601	CTTCTCGAAACCTTCCCGGAAAGGTATGCGGTGTGAAATACCGCACAGATGCGTAAAGGAGA	660
661	AAATACCGATCAGGGCGCTTCCCGCTTCTCGCTCACTGACTCGCTGCGCTCGGTGGT	720
661	AAATACCGATCAGGGCGCTTCCCGCTTCTCGCTCACTGACTCGCTGCGCTCGGTGGT	720
721	CGGCTCGGGCGAGCGGTATCAGCTCACTCAAAGGGCGGTAATACGGTTATTCACAGAAATCA	780



Db 1801 ACTGATCGAAAAATAACCGCTCGTAAAGATAACGAAAGGAATGTCTCTCTAAGGTATA 1860  
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Db 1861 TAAGCTGGTGGGAAAAATGAATAACCTATATTTAAAAATGACGACAGCGCGGTATAAAGG 1920  
QY 1921 GACCACTTATGATGTGAAACGGGAAAAAGGACATGATGCTATGCTGGAAGAAAGCTGCC 1980  
Db 1921 GACCACTTATGATGTGAAACGGGAAAAAGGACATGATGCTATGCTGGAAGAAAGCTGCC 1980  
QY 1981 TGTTCAAAAGGTCTGCACTTTGAAACGGCATGATGCTGAGCAATCTGCTCATGAGTGA 2040  
Db 1981 TGTTCAAAAGGTCTGCACTTTGAAACGGCATGATGCTGAGCAATCTGCTCATGAGTGA 2040  
QY 2041 GGCCGATGGCGTCTCTTGGCTCGGAAGAGTATGAAGATGAACAAAGCCCTGAAAAGATTAT 2100  
Db 2041 GGCCGATGGCGTCTCTTGGCTCGGAAGAGTATGAAGATGAACAAAGCCCTGAAAAGATTAT 2100  
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Db 2101 CGAGCTGATGCGGAGTGCATCAGGCTCTTTCACTCCATCGACATATCGGATTTGTCCCTA 2160  
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Db 2161 TACGAATAGCTTAGACAGCGCTTAGCCGAATTTGGATTACTTACTGAAATAACGATCTGGC 2220  
QY 2221 CGATGTGATTTGCGAAACCTGGGAAGAGACACTCCATTTAAAGATCGCGCGAGCTGTA 2280  
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Db 2341 AGACAGCAACATCTTTGTGAAAGATGCGAAAGTAAGTGGCTTTATTTGATCTCGGGAAG 2400  
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Db 2401 CGCAGGCGGACAAAGTGGTATGACATTTGCTGCTCGCTCCGCTCGATCAGGAGGATAT 2460  
QY 2461 CGGGGAAGAACAGTATGTGAGCTATTTTTTGACTTACTCGGGATCAAGCCTGATTTGGGA 2520  
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QY 2581 ATCCGCGGACAAAGGAGCGCACCGACTTCTTCCGCATCAAGTGTCTTGGCTCTCAGG 2640  
Db 2581 ATCCGCGGACAAAGGAGCGCACCGACTTCTTCCGCATCAAGTGTCTTGGCTCTCAGG 2640  
QY 2641 CCAGGCGCCACGGCAAGTATTTGGGCAAGGGGTGCTGTTGATTTCTGTCAGGCGCAAGATTC 2700  
Db 2641 CCAGGCGCCACGGCAAGTATTTGGGCAAGGGGTGCTGTTGATTTCTGTCAGGCGCAAGATTC 2700  
QY 2701 GGAATACCAAGTACGAGAAGGACGGCCAGACGCTCTACGGGACCGACTTCAATTTCCCGATA 2760  
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QY 3721 TCGACGAGGAAATCGTCTGCTGTTTGTGGGACCACTACACGAAATTCATATGGGAGA 3780  
Db 3721 TCGACGAGGAAATCGTCTGCTGTTTGTGGGACCACTACACGAAATTCATATGGGAGA 3780  
QY 3781 AGTACCGCAAGCTGTCCGACGCGCCGACGAGTGTTCGACTATTTTCAGCTCGCACCGGG 3840  
Db 3781 AGTACCGCAAGCTGTCCGACGCGCCGACGAGTGTTCGACTATTTTCAGCTCGCACCGGG 3840  
QY 3841 AGCCGTACCCGCTCAAGCTTGGAAAACTTCCGCTCATGTGCGGATTCACCCGCG 3900  
Db 3841 AGCCGTACCCGCTCAAGCTTGGAAAACTTCCGCTCATGTGCGGATTCACCCGCG 3900  
QY 3901 TGAAGAAGTGGCGCGAGCAGGTGCGGAAAGCCTCGGAAGAGTTTGGAGGACGCGGCTGG 3960  
Db 3901 TGAAGAAGTGGCGCGAGCAGGTGCGGAAAGCCTCGGAAGAGTTTGGAGGACGCGGCTGG 3960  
QY 3961 TGAACACGCTGGGTCAATGATGACCTTGGTGAATTTGCAAAACGCTTAGGGCCTTTGGGGT 4020  
Db 3961 TGAACACGCTGGGTCAATGATGACCTTGGTGAATTTGCAAAACGCTTAGGGCCTTTGGGGT 4020

Qy	4021	CAGTTCGGCTGGGGTTTCAGCAGCCAGCGCTTTACTGCGCATTTCTAGGTTGACGCTT	4080
Db	4021		4080
Qy	4081	CTGATGGGCTGCCCTGTATCAGTGGTGATTTGTGCCGAGCTGCCGTCGGGGAGCTGTT	4140
Db	4081		4140
Qy	4141	GGCTGGCTGGCAGGATATATTGTGGTGAACAAATTGACGCTTAGACAACCTTAATA	4200
Db	4141		4200
Qy	4201	ACACATTGCGGACGTTTTTAAATGACTGGGCTATCCCCGGGGATATCCATAGGCCCG	4260
Db	4201		4260
Qy	4261	ATCTAGTAACATAATGACACCGCGCGGATAAATTTATCCTAGTTTGGCGCTATATTTTG	4320
Db	4261		4320
Qy	4321	TTTTCTATCGGTAATTAATGTAATAATGCGGACTCTAATCATATAAAACCCATCTCATA	4380
Db	4321		4380
Qy	4381	AATAACCTCATGCAATTACATGTTAATTATTACATGCTTAACGTAATTCACAGAAATTAT	4440
Db	4381		4440
Qy	4441	ATGATAATCATCGCAAGACCGGCAACAGGATTCAATCTTAAGAACTTTATTGCCAAATG	4500
Db	4441		4500
Qy	4501	TTTGAACGATCGTTCGTGAGCTATGGCCCGA	4533
Db	4501		4533

Result No.	Score	Query		DB	ID	Description
		Match	Length			
C	1	2536.2	52.8	12241	4	US-09-548-138-4
	2	2222.2	52.5	13737	4	US-09-538-414-10
	3	2222.2	52.5	13737	4	US-10-074-279-10
	4	1393	29.0	10323	3	US-09-280-428A-11
	5	1393	29.0	14113	3	US-09-223-134-1
	6	1393	29.0	14113	3	US-08-992-801-1
	7	1393	29.0	14113	3	US-09-223-535-1
	8	1025.2	21.3	4161	4	US-09-185-244-8
	9	1025.2	21.3	4161	4	US-09-471-513-1
	10	807	16.8	856	4	US-09-171-517B-15
C	11	795	16.5	795	4	US-09-134-000C-3304
	12	618.6	12.9	10323	4	US-09-280-428A-11
	13	618.6	12.9	14113	3	US-09-223-134-1
	14	618.6	12.9	14113	3	US-08-992-801-1
	15	618.6	12.9	14113	3	US-09-223-535-1
	16	593.2	12.3	4557	4	US-08-778-717-5
	17	592.8	12.3	5234	2	US-08-992-334-2
	18	592.8	12.3	5234	3	US-08-302-752-2
	19	592	12.3	3123	3	US-09-042-353-152
	20	592	12.3	3123	4	US-08-758-417A-416
C	21	592	12.3	3516	4	US-09-058-483-9
	22	592	12.3	3699	1	US-08-053-131-120
	23	592	12.3	3699	1	US-08-645-641-120
	24	592	12.3	3699	1	US-07-853-408B-120
	25	592	12.3	3699	1	US-08-096-762-120
	26	592	12.3	3699	2	US-08-308-865-120
	27	592	12.3	3699	5	PCR-US92-10983-120





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; APPLICANT: Kendra, D.
; APPLICANT: Reinders, J.
; APPLICANT: Kuznia, R.
; APPLICANT: Dill-Mackey, R.
; TITLE OF INVENTION: Transgenic Plant and Methods
; FILE REFERENCE: sequencelist
; CURRENT APPLICATION NUMBER: US/09/538,414
; CURRENT FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 13737
; TYPE: DNA
; ORGANISM: Plasmid
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Plasmid
US-09-538-414-10

Query Match      52.5%; Score 2522.2; DB 4; Length 13737;
Best Local Similarity 76.5%; Pred. No. 0;
Matches 3505; Conservative 0; Mismatches 558; Indels 518; Gaps 13;

Qy      1  CCGGGCTGGTTCCTCGCGCTGGGCTGGCGGCGCTATGGCCCTGCAAAACGCGCAG 60
Db      4371 CCGGGCTGGTTCCTCGCGCTGGGCTGGCGGCGCTATGGCCCTGCAAAACGCGCAG 4430

Qy      61  AAGCCGCTGAAGCCGTGTGCGAGACACG- - - - -CGGCCGCGCGGCTGTGTGATACCTC 116
Db      4431 AAGCCGCTGAAGCCGTGTGCGAGACACCGCGCGCGCGCGGCGTGTGTGATACCTC 4490

Qy      117 GCGGAAACCTGGCCCTCACTGACAGATGAGGGCGGACGTTGACACTTGAGGGCGCGAC 176
Db      4491 GCGGAAACCTGGCCCTCACTGACAGATGAGGGCGGACGTTGACACTTGAGGGCGCGAC 4550

Qy      177 TCACCCGCGCGCGGTTCACAGATGAGGGCGAGGCTCGAATTCGCGCGCGCACGTGGAGC 236
Db      4551 TCACCCGCGCGCGGTTCACAGATGAGGGCGAGGCTCGAATTCGCGCGCGCACGTGGAGC 4610

Qy      237 TGCCACGCTCGCAATTCGGGCAAAACGCTGATTTACGCGAGTTTCCACAGATGATG 296
Db      4611 TGCCACGCTCGCAATTCGGGCAAAACGCTGATTTACGCGAGTTTCCACAGATGATG 4670

Qy      297 TGACACGCTGGGGTAAGTGCCTCGGCTATTGACACTTGAGGGCGGCGACTACTGAC 356
Db      4671 TGACACGCTGGGGTAAGTGCCTCGGCTATTGACACTTGAGGGCGGCGACTACTGAC 4730

Qy      357 AGATGAGGGCGCGCATCTTGACACTTGAGGGCGAGAGTGTGACAGATGAGGGCGCGAC 416
Db      4731 AGATGAGGGCGCGCATCTTGACACTTGAGGGCGAGAGTGTGACAGATGAGGGCGCGAC 4790

Qy      417 CTATTGACATTTGAGGGCTGTCCACAGGCAAGAAATCCAGCATTTGCAAGGGTTTCGCG 476
Db      4791 CTATTGACATTTGAGGGCTGTCCACAGGCAAGAAATCCAGCATTTGCAAGGGTTTCGCG 4850

Qy      477 CCGTTTTTCGCGCACCGCTAACCTGTCTTTTAACTGCTTTTAAACCAATTTTATAAAC 536
Db      4851 CCGTTTTTCGCGCACCGCTAACCTGTCTTTTAACTGCTTTTAAACCAATTTTATAAAC 4910

Qy      537 CTTGTTTTTAAACAGGGCTGCGCCCTGTGCGCTGACCGCGCACCGCAAGGGGGGTGCC 596
Db      4911 CTTGTTTTTAAACAGGGCTGCGCCCTGTGCGCTGACCGCGCACCGCAAGGGGGGTGCC 4970

Qy      597 CCCCCTTCTCGAAACCTCCCGG- - - - - 618
Db      4971 CCCCCTTCTCGAAACCTCCCGGCGGCTTAACGCGGCGCTCCCATCCCGGCGGCTGCG 5030

Qy      619 - - - - - 649
Db      5031 CCCCCTCGCGCGCAACGCGCTCAACCCCAAAATGGCAGCGTGGCAGTCTTGGCAATTGC 5090

Qy      650 GCGTAAGGAGAAAATACCGATACGGGCGCTCTTCGCTTCTCGCTCACTGACTCGCTGC 709
Db      5091 CCGGATCGGGCAGTAACGGGATGGCGATCAGCCCGGACGCGCGCGCAAGCATTTGA 5150
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Qy      710 GCTCGGTTCGTTTCGGCTCGCGGAGCGGTATCAGCTCACTCAAAGCGGTAATACGTTAT 769
Db      5151 CGTCCGCGAGGTGCTGCGATCGCATTCAGCGACAGGTCCCGGCAAGTGAAGGCGCGG 5210

Qy      770 CC- - - - - 771
Db      5211 CTTGGGTGGGCGCTGCCCTTCACTTTCGGGCGTGGGCGCATTCACGGAATTCATGCGGG 5270

Qy      772 - - - - - 771
Db      5271 GCGGCAATTTTACCTTGGGCATTTCTTGGCATATGTCGTCAGTGTGCGGGTGCCTGCTCGTGT 5330

Qy      772 - - - - -ACAGAAATCAGGGGATACAGGAGAAACAAACATGTGAG 808
Db      5331 CCGGGGTGCGATAAACCCAGCAACCATTTGAGTGATAGGTAAAGATTATACCGAGTAT 5390

Qy      809 CAAAAGG- - - - - 815
Db      5391 GAAACAGGAATTTGGACCTTTACAGAAATTAATCTATGAAGCGCATATTTAAAGAGCTAC 5450

Qy      816 - - - - - 815
Db      5451 CAAGACGAGAGGATGAAGAGGATGAGAGGCGAGATTGCTTGAATATATTGACAACTACT 5510

Qy      816 - - - - -CCAGCAAAAGGCGCAGGAACCGTAAAGGCGGTTTCTGGCGCTTT 861
Db      5511 GATAAGATAATATATCTTTTATATAGAGATATCGCGTATGTAAGGATTTACAGGGGCA 5570

Qy      862 TTCATAGGCTCGGC- - - - - 876
Db      5571 AGCATAGGCGCGCTTATCAATATATCTATAGAATGGCAAGCATAAAACTTGCA 5630

Qy      877 - - - - -CCCCCTGACGAGCATCAAAATTCGACGCTCAAGTCAGAGGTG 920
Db      5631 TGGACTAAATGCTTGAACCCAGGACAAATAACCTTATAGCTTGTAAATTTCTATCATAATTG 5690

Qy      921 GCGAAACCCGACAG- - - - - 934
Db      5691 GGTAATGACTCCAACTATTGATAGTGTGTTTATGTCAGATAATGCCCGATGACTTTGTC 5750

Qy      935 - - - - -GACTATAAAGATACACGAGCGTTTCCCTCGGAAGCTCCCTGTCGCGC 981
Db      5751 ATGACGCTCCACCGAATTTTGAGAAACGACAGCACTTCGCTCCAGCGCTGCCAGTCTG 5810

Qy      982 TCTCTGTTCCGACCTGCGCGCT- - - - -TACCGGATACCTGTCGCGCTTTCTCCCTTCGGAAG 1040
Db      5811 CCTCAGATTTCAGGTTATGCGCGCTCAATTCGCTCGTATATCGCTTGTGATTACGTGCGAG 5870

Qy      1041 CGTGGCGCTTCTCATAGCTCACGCTGATAGGTATCTCAGTTTCGTTGAGGTTCGTTGCTC 1100
Db      5871 CTTTCCCTTCAGGGGGAATTCATACGCGGCGAGCATCCGTCATCATATCACCACGTC 5930

Qy      1101 CAAGCTGGGCTGTGTGCACGAA- - - - -CCCCCGGTTTCAGCCCGCAGCCGCTGCGCTTATCC 1155
Db      5931 AAGGGTGACAGCAGGCTCATAGACGCCCGCAGCGTCGCCATAGTGGCTTCCACGAATAC 5990

Qy      1156 GGTAACTATCGTTGAGTCCAAACCCGGTAAGACACACTTTATGCGCACTTGGCAGCAGCC 1215
Db      5991 GTGCGCAACCAACCGCTTTCGGGAGACTGTCTATCGCGTAAACACAGCCAGCGCTGGCGCGA 6050

Qy      1216 TTCTACCATTAATCCGCGATAAACCCAGCGAAACCATTTGAGTGATAGGTAAAGATTATACC 1275
Db      6051 TTTAGCCCCCAGCATAGCCCCCA- - - - -CTGTTTCGTCATTTCCCGGCGAGCATGACGCTACTG 6108

Qy      1276 GAGTATGAAACAGAAATTTGGACCTTTTACAGAAATTAATCTATGAAGCGCATATTTAAA 1335
Db      6109 CCGGCTGTATGCGGAGGTTACCGACTGCGGCTGAGTTTAAAGTGAAGTAAATTCG 6168

Qy      1336 AAGTACCAAGACGAGAGGATGAAGAGGATGAGGAGGAGATGCGCTTGAATATATGA 1395
Db      6169 TGTAGGCCCAACGCCCATTAATCGGGCTGTGTCGCGGCAATCCCAACGCCCATTCATGGCCA 6228
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Qy	1396	CAATCTGATAAGATAATACATCTTTTATATAGAGATAT-----CGCGTATGT	1445
Db	6229	TATCAATGATTTTCTGGTGGCTACCGGGTTGAGAAGCGGTGAAGTGAACTGCAGTTGCC	6288
Qy	1446	AAGGATTTACGGGGCAAGCATAGGCAGCGC-----	1477
Db	6289	ATGTTTTACGGCAGTGAGACGAGATAGCGCTGATGTCGGGGTGCCTTTTGGCCGTTAC	6348
Qy	1478	-----GCTTATCAATATATCTATAGAAATGGGCAAAAGCATATAAAACCTT-----GCATGGAC	1527
Db	6349	GCACCACCCGTCAGTAGCTGACACAGAGGGAAGCTGATAGACACAGAAGCCACTGGAG	6408
Qy	1528	TAATGCTTGAACCCAGGACA---ATAACCTTATAGCTTGTAAATCTCAATAAATTTGTG	1584
Db	6409	CACCTCAAAAACCAATACATACATAAATCAGTAAGTTGGCAGCATCACCCATAAATTTGTG	6468
Qy	1585	GTITCAAAATCCGCTCCGTCGATCTATGTATACGCCAATTTGAAAACCACTTTGAAA	1644
Db	6469	GTITCAAAATCCGCTCCGTCGATCTATGTATACGCCAATTTGAAAACCACTTTGAAA	6528
Qy	1645	AAGCTGTTTTCTGGTATTTAAGGTTTTAGAAATGCAAGGAAACAGTGAATTTGGAGTTCTCT	1704
Db	6529	AAGCTGTTTTCTGGTATTTAAGGTTTTAGAAATGCAAGGAAACAGTGAATTTGGAGTTCTCT	6588
Qy	1705	TGTTATAATTAGCTTTCTGGGTATCTTTAAATCTGTAGAAAGAGGAAATAATA	1764
Db	6589	TGTTATAATTAGCTTTCTGGGTATCTTTAAATCTGTAGAAAGAGGAAATAATA	6648
Qy	1765	AATGGCTAAATGAGATATCACCGGAATTTGAAAACCTGATCGAAAATACCGTCCGT	1824
Db	6649	AATGGCTAAATGAGATATCACCGGAATTTGAAAACCTGATCGAAAATACCGTCCGT	6708
Qy	1825	AAAAGATACGGAAGGATGCTCTCTCTAAGGTATATAAGCTGGTGGGAGAAAATGAAA	1884
Db	6709	AAAAGATACGGAAGGATGCTCTCTCTAAGGTATATAAGCTGGTGGGAGAAAATGAAA	6768
Qy	1885	CCTATATTTAAAATAGCAGCAGCCGGTATAAGGGACCACCTATGATGTGGAACGGGA	1944
Db	6769	CCTATATTTAAAATAGCAGCAGCCGGTATAAGGGACCACCTATGATGTGGAACGGGA	6828
Qy	1945	AAAGGACATGCTATGGCTGGAAGGAAAGCTGCCTGTTCCAAAGTCTCTGCACITTTGA	2004
Db	6829	AAAGGACATGCTATGGCTGGAAGGAAAGCTGCCTGTTCCAAAGTCTCTGCACITTTGA	6888
Qy	2005	ACGCGATGATGGCTGGAGCAATCTGCTCATGAGTGAGGCGGATGGCGTCTTTGCTCGGA	2064
Db	6889	ACGCGATGATGGCTGGAGCAATCTGCTCATGAGTGAGGCGGATGGCGTCTTTGCTCGGA	6948
Qy	2065	AGAGTATGAAGATGAACAAAGCCCTGAAAAGATTATCGAGCTGTATGCGGAGTGCAATCAG	2124
Db	6949	AGAGTATGAAGATGAACAAAGCCCTGAAAAGATTATCGAGCTGTATGCGGAGTGCAATCAG	7008
Qy	2125	GCTCTTTCACTCCATCGACATATCGGATTTGTCCTTATACGAATAGCTTAGACAGCCGCTT	2184
Db	7009	GCTCTTTCACTCCATCGACATATCGGATTTGTCCTTATACGAATAGCTTAGACAGCCGCTT	7068
Qy	2185	AGCGGAATTCGATTACTGTAATACGATCTGGCCGATGTGGATTTCGAAAACCTGGGA	2244
Db	7069	AGCGGAATTCGATTACTGTAATACGATCTGGCCGATGTGGATTTCGAAAACCTGGGA	7128
Qy	2245	AGAAGACACTCCATTTAAAGATCCGCGAGCTGTATGATTTTTTAAAGACGGAAGGCC	2304
Db	7129	AGAAGACACTCCATTTAAAGATCCGCGAGCTGTATGATTTTTTAAAGACGGAAGGCC	7188
Qy	2305	CGAAGAGAACTTGTCTTTTCCACCGCGACCTGGGAGACAGCAACATCTTTGTGAAGA	2364
Db	7189	CGAAGAGAACTTGTCTTTTCCACCGCGACCTGGGAGACAGCAACATCTTTGTGAAGA	7248
Qy	2365	TGCAAAAGTAAGTGGCTTTATTCATCTTGGAGAGAGCGGACGAGGAGTGGTATGA	2424
Db	7249	TGCAAAAGTAAGTGGCTTTATTCATCTTGGAGAGAGCGGACGAGGAGTGGTATGA	7308
Qy	2425	CATTGCCCTTCTGGCTCCGGTCGATCAGGGAGGATATCGGGGAAGAACAGTATGTCGAGCT	2484

Db	7309	CATTGCCCTTCTGGCTCCGGTCGATCAGGGAGGATATCGGGAAAGAACAGTATGTCGAGCT	7368
Qy	2485	ATTTTTTGACTTACTCGGGATCAAGCTGATTCGGAGAAATAAATAATATATATTTTACT	2544
Db	7369	ATTTTTTGACTTACTCGGGATCAAGCTGATTCGGAGAAATAAATAATATATATTTTACT	7428
Qy	2545	GGATGAATTTGTTTAGTACCTAGATGTGGCGCAACGATGCGGCGACAAGCAGAGAGCGCA	2604
Db	7429	GGATGAATTTGTTTAGTACCTAGATGTGGCGCAACGATGCGGCGACAAGCAGAGAGCGCA	7488
Qy	2605	CCGACTTCTTCCGATCAAGTGTTCGCTCTCAGGCCGAGGCCCAAGGAAATTTTGG	2664
Db	7489	CCGACTTCTTCCGATCAAGTGTTCGCTCTCAGGCCGAGGCCCAAGGAAATTTTGG	7548
Qy	2665	GCAGGGTCTCGTGTATTCTGTCAGGGCAAGATTCGGAATACCAAGTACGAGAGAGACG	2724
Db	7549	GCAGGGTCTCGTGTATTCTGTCAGGGCAAGATTCGGAATACCAAGTACGAGAGAGACG	7608
Qy	2725	GCAGAGCGGTCTACGGGACCGACTTTCATTTGCCGATTAAGGTGGATTATCTCGACACCAAGG	2784
Db	7609	GCAGAGCGGTCTACGGGACCGACTTTCATTTGCCGATTAAGGTGGATTATCTCGACACCAAGG	7668
Qy	2785	CACAGCGGGTCAAATCAGGAATAAGGGCACATTTGCCCGCGTGTAGTCTGGGCAATCC	2844
Db	7669	CACAGCGGGTCAAATCAGGAATAAGGGCACATTTGCCCGCGTGTAGTCTGGGCAATCC	7728
Qy	2845	CGCAAGAGGGTCAATCAATTCGGACCTTTGACCGGAGGCGATACAGGCAAGAACTGATCG	2904
Db	7729	CGCAAGAGGGTCAATCAATTCGGACCTTTGACCGGAGGCGATACAGGCAAGAACTGATCG	7788
Qy	2905	ACGCGGGTTCGCGGAGGATGCGCAACCACTCGCAAGCCGACCGTCATCGTCTGCGC	2964
Db	7789	ACGCGGGTTCGCGGAGGATGCGCAACCACTCGCAAGCCGACCGTCATCGTCTGCGC	7848
Qy	2965	CCCGGAAACCTTTCAGTCCGTCCGTTCGATGTCCAGCAAGCTACGGCCAAAGATCAGC	3024
Db	7849	CCCGGAAACCTTTCAGTCCGTCCGTTCGATGTCCAGCAAGCTACGGCCAAAGATCAGC	7908
Qy	3025	GGCAGAGCTGCAACTCCCTCCCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGTT	3084
Db	7909	GGCAGAGCTGCAACTCCCTCCCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGTT	7968
Qy	3085	CGCGTCTCTCGAAACAGGAGGCGCGAGTTTGGCGAAGTCGATGACCATCGACACGCGAG	3144
Db	7969	CGCGTCTCTCGAAACAGGAGGCGCGAGTTTGGCGAAGTCGATGACCATCGACACGCGAG	8028
Qy	3145	GAACTATGACGACCAAGAGCGAAAAACCGCGCGGAGGACCTGGCAAAAACAGGTCAGCG	3204
Db	8029	GAACTATGACGACCAAGAGCGAAAAACCGCGCGGAGGACCTGGCAAAAACAGGTCAGCG	8088
Qy	3205	AGGCCAAGCAGCGCGTTGCTGAAACACACGAGCAGCAGATCAGGAAATCGAGCTTT	3264
Db	8089	AGGCCAAGCAGCGCGCGTTGCTGAAACACACGAGCAGCAGATCAGGAAATCGAGCTTT	8148
Qy	3265	CCTTGTTCGATATTTGCGCGTGGCGGACACGATGCGAGCGATGCGCAAAACAGCGCCC	3324
Db	8149	CCTTGTTCGATATTTGCGCGTGGCGGACACGATGCGAGCGATGCGCAAAACAGCGCCC	8208
Qy	3325	GCTCTCCCTGTTTACACGCGCAACAAGAAAATTCGCGCGAGGCGCTCGAAAACAGG	3384
Db	8209	GCTCTCCCTGTTTACACGCGCAACAAGAAAATTCGCGCGAGGCGCTCGAAAACAGG	8268
Qy	3385	TCAATTTTCCAGCTCAACAGGAGCTGAAGTACCTTACACCGGGCTCGAGCTCGGGCCG	3444
Db	8269	TCAATTTTCCAGCTCAACAGGAGCTGAAGTACCTTACACCGGGCTCGAGCTCGGGCCG	8328
Qy	3445	ACGATCAAGAACTGGTGTGGCAGCAGGTGTGGAGTACGGAAGCGCACCCCTATCGGCG	3504
Db	8329	ACGATCAAGAACTGGTGTGGCAGCAGGTGTGGAGTACGGAAGCGCACCCCTATCGGCG	8388
Qy	3505	AGCCGATCACCTTTCAGCTTCTACGAGCTTTGCCAGGACCTTGGCTGGTCAATCAATGGCC	3564



QY 816 -----CCAGCAAAAGGCCAGGAAACCGTAAAAAGGCCGGCTTCTGCTGGCGTTT 861  
Db GATAAGATAATATATCTTTTATATAGAAAGATATCGCGGTATGTAAGGATTTTCAGGGGGCA 5570  
QY 862 TTCATAGGCTCCGC----- 876  
Db AGGCATAGGCGCGCTTATCAATATATCTATAGAAATGGCAAGCATAAAACTTGC 5630  
QY 877 -----CCCCTGACGAGCATCAAAAAATCGAGCTCAAGTCAAGAGGTG 920  
Db TGGACTAATGCTTGAAACCCAGGACAATAACCTTATAGCTTGTAAATCTCATATAATG 5690  
QY 921 GCGAAACCCGACAG----- 934  
Db GGTAATGACTCCAACCTTATTGATAGTGTATTTATGTTTTCAGATAAATGCCCGATGACTTTGTGTC 5750  
QY 935 -----GACTATAAAGTACCAGCGTTTCCCTCGGAAGCTCCCTCGTGGC 981  
Db ATGAGCTCCACCGATTTTGGAGAACGACAGCACTTCCGTCACGCGGTGCCAGGTGCTG 5810  
QY 982 TCTCCTGTTCCGACCCCTGCGCT- TACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAG 1040  
Db CCTCAGATTGAGTTATGCGCTCAATTCCGCTGGTATATCGCTTGTGATAGTGCAG 5870  
QY 1041 CGTGGCGCTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTGCTTCCGCTC 1100  
Db CTTTCCCTTCAGGCGGATTCATACAGCGGCCAGCCATCCGTATCCATATCACCCAGTCC 5930  
QY 1101 CAAGCTGGGTGTGTGCAAGAA-----CCCCCGTTTCAGCCCGACCGCTCGCTTATCC 1155  
Db AAGGGGTGACAGCGGCTCATAGACGCCCGCCAGCGTCGCCATAGTGGCTTCACCGAATAC 5990  
QY 1156 GGTAACTATCGTTGAGTCCAAACCCGGTAAGACACAGACTTATCGCCACTGGCAGAGCC 1215  
Db GTGGGAAACAAACGCTTTCGGAGACTGTCTACGGGTAAACAGCCAGCGCTGGCGCA 6050  
QY 1216 TTCTACCATATCCGGATAAACCCAGCGAACCATTTGAGGTGATAGGTAAAGATATATACC 1275  
Db TTTAGCCCCGACATAGCCCCA--CTGTTCTGTCATTTCGCGCAGACGATGACGTCACTG 6108  
QY 1276 GAGGTATGAAACAGAAATTTGGACCTTTACAGAAATTAATCTATGAAAGCGCCATATTTAA 1335  
Db CCGGCTGTATGCGCGAGGTACCGACTGCGGCTGAGTTTTTAAAGTGACGTAATAATCG 6168  
QY 1336 AAGCTACCAAGACGAAGAGATCAAGAGGATGAGGAGCAGATTGCTTGAATATATGA 1395  
Db TGTGAGGCCAACGCCATTAATGCGGCTGTTGCCGGCATCCAAAGCCATTCATGGCCA 6228  
QY 1396 CAATACCTGATAAGATAATACATCTTTTATATAGAAGATAT------CGCGGTATGT 1445  
Db TATCAATGATTTTCTGTGCTGCTACCGGTTGAGAAGCGGTGTAAGTGAACCTGCACTGCC 6288  
QY 1446 AAGGATTTACGGGGCAAGGCATAGGCAGCGC----- 1477  
Db ATGTTTTACGGCAGTGAGAGCAGATGAGCGCTGATGTCGCGGCTGCTTTTCCCGTTAC 6348  
QY 1478 -----GCTTATCAATATATCTATAGAAATGGCAAGCAATAAACTT-----GCATGGAC 1527  
Db GCACCAACCCGCTCAGTAGCTGAACAGAGGGAACAGTGTAGACACAGAACCCACTGGAG 6408  
QY 1528 TAATGCTTGAACCCAGGACA---ATAAACCTTATAGCTTGTAAATTTCTACCAAAATTTGTG 1584  
Db CACCTCAAAAACCATCATACACTAAATCAGTAAGTTGGCAGCATCAACCCATAATTTGTG 6468  
QY 1585 GTTTCAAAATCGGCTCGTATCTATGTAATGCGCAACCTTTGAAAAACAACCTTTGAAA 1644  
Db GTTTCAAAATCGGCTCGTATCTATGTAATGCGCAACCTTTGAAAAACAACCTTTGAAA 6528  
QY 1645 AAGCTGTTTCTGATTTTAAAGTTTATAGATCAAGGACAGTGAATTTGGAGTTGCTCT 1704  
Db AAGCTGTTTCTGATTTTAAAGTTTATAGATCAAGGACAGTGAATTTGGAGTTGCTCT 6588

QY 1705 TGTATAAATTAGCTTCTTGGGTATCTTTAAATACCTGTAGAAAAGAGAAAGAAATAATA 1764  
Db TGTATAAATTAGCTTCTTGGGTATCTTTAAATACCTGTAGAAAAGAGAAAGAAATAATA 6648  
QY 1765 AATGGCTAAAATCAGAAATATCACCGGAATTTGAAAAAATGATCGAAAAATACCGCTCGCT 1824  
Db AATGGCTAAAATCAGAAATATCACCGGAATTTGAAAAAATGATCGAAAAATACCGCTCGCT 6708  
QY 1825 AAAAGATACGGAAGGAATGTCTCTCTAAGGTATATAAGCTGTGGGAGAAAAATGAAA 1884  
Db AAAAGATACGGAAGGAATGTCTCTCTAAGGTATATAAGCTGTGGGAGAAAAATGAAA 6768  
QY 1885 CCTATATTTAAAAATGACGAGCCGCTATATAAGGGAACCACTATGATGTGAAACGGGA 1944  
Db CCTATATTTAAAAATGACGAGCCGCTATATAAGGGAACCACTATGATGTGAAACGGGA 6828  
QY 1945 AAGGACATCATGCTATGCTGGAAGGAAGCTGCTGTTTCCAAAGGTCCTGCACCTTGA 2004  
Db AAGGACATCATGCTATGCTGGAAGGAAGCTGCTGTTTCCAAAGGTCCTGCACCTTGA 6888  
QY 2005 ACGGCATGATGCTGGAGCAATCTGCTCATGAGTGAGGCGCATGGGCTCTCTTGTCTCGGA 2064  
Db ACGGCATGATGCTGGAGCAATCTGCTCATGAGTGAGGCGCATGGGCTCTCTTGTCTCGGA 6948  
QY 2065 AGAGTATGAAGATGAACAAAGCCCTGAAAGATTATCGAGCTGTATGCGGAGTGCAATCAG 2124  
Db AGAGTATGAAGATGAACAAAGCCCTGAAAGATTATCGAGCTGTATGCGGAGTGCAATCAG 7008  
QY 2125 GCTCTTTTCACTCCATCGACATATCGGATTTGTCCTATACGAATAGCTTAGACAGCCGCTT 2184  
Db GCTCTTTTCACTCCATCGACATATCGGATTTGTCCTATACGAATAGCTTAGACAGCCGCTT 7068  
QY 2185 AGCCGAATTTGGATTTACTTCTGAATAACGATCTGGCCGATGTGGATTGCGAAAACTGGGA 2244  
Db AGCCGAATTTGGATTTACTTCTGAATAACGATCTGGCCGATGTGGATTGCGAAAACTGGGA 7128  
QY 2245 AGAAGACATCCATTTAAAGATCCGCGCAGCTGTATGATTTTTTAAAGACGAAAAAGCC 2304  
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QY 2305 CGAAGGAACTTGTCTTTTCCACGCGACCTGGGAGACAGCAACATCTTTTGTGAAGA 2364  
Db CGAAGGAACTTGTCTTTTCCACGCGACCTGGGAGACAGCAACATCTTTTGTGAAGA 7248  
QY 2365 TGGCAAGTAAGTGGCTTTTATTGATCTTGGGAGAACGCGCAGGCGGCAAGTGGTATGA 2424  
Db TGGCAAGTAAGTGGCTTTTATTGATCTTGGGAGAACGCGCAGGCGGCAAGTGGTATGA 7308  
QY 2425 CATTCCTTCTCGCTCCGTCGATCAGGAGGATATCGGGGAGAAACAGTATGTCAGCT 2484  
Db CATTCCTTCTCGCTCCGTCGATCAGGAGGATATCGGGGAGAAACAGTATGTCAGCT 7368  
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Db ATTTTGTACTTCTGGGATCAAGCTGATTTGGGAGAAAAATAAATATATATTTTACT 7428  
QY 2545 GGATGAATTTTGTACTTCTAGTGTGCGCAACGATCGCGGCAACAGCAGGAGCGCA 2604  
Db GGATGAATTTTGTACTTCTAGTGTGCGCAACGATCGCGGCAACAGCAGGAGCGCA 7488  
QY 2605 CCGACTTCTTCGCAATCAAGTGTTTTGGCTCTCAGGCGGAGGCCACGCAAGTATTTGG 2664  
Db CCGACTTCTTCGCAATCAAGTGTTTTGGCTCTCAGGCGGAGGCCACGCAAGTATTTGG 7548  
QY 2665 GCAAGGGTCTGCTGATTTCTGTCAGGGCAAGATTCCGGAATACCAAGTACGAGAACGACG 2724  
Db GCAAGGGTCTGCTGATTTCTGTCAGGGCAAGATTCCGGAATACCAAGTACGAGAACGACG 7608  
QY 2725 GCCAGACGCTTACGCGGACCGACTTCTTATGTCGATAGGTGATTTATCTGGACACCAAGG 2784  
Db GCCAGACGCTTACGCGGACCGACTTCTTATGTCGATAGGTGATTTATCTGGACACCAAGG 7668  
QY 2785 CACCAGGCGGTCAAATCAGGAATAAGGGCACATTTGCCCGCGCTGAGTCGGGGCAATCC 2844





Db 6272 AGGCATACGCGAAGAACTGATCGACGCGGGTTTTCGCGCGAGGATGCGCAAAACCATCG 6213  
Qy 2941 CAAGCCGCAACGTCATCGCTGCGCCCGCGAAACCTTCCAGTCGCTCGCTCGATGGTCC 3000  
Db 6212 CAAGCCGCAACGTCATCGCTGCGCCCGCGAAACCTTCCAGTCGCTCGATGGTCC 6153  
Qy 3001 AGCAAGCTACGCGCAAGATCGAGCGGACACGCTGCAACTGGCTCCGCCCTCGCCCTGCCCG 3060  
Db 6152 AGCAAGCTACGCGCAAGATCGAGCGGACACGCTGCAACTGGCTCCGCCCTCGCCCTGCCCG 6093  
Qy 3061 CGCCATCGCGCGCGCTGGAGCGTTTCGCTGCTCTCGAAAGAGGCGGCGAGTTTGGCGA 3120  
Db 6092 CGCCATCGCGCGCGCTGGAGCGTTTCGCTGCTCTCGAAAGAGGCGGCGAGTTTGGCGA 6033  
Qy 3121 AGTCGATGACATCGACACGCGAGGAACTATGACGACCAAGAGCGGAAAAACCGCGCGG 3180  
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Qy 3181 AGGACCTGGCAAAACAGGTGAGCGAGGCGCAAGCGGCGGCTTGTCTGAAACACACGAAGC 3240  
Db 5972 AGGACCTGGCAAAACAGGTGAGCGAGGCGCAAGCGGCGGCTTGTCTGAAACACACGAAGC 5913  
Qy 3241 AGCAGATCAAGGAAATCGAGCTTTCCTTGTTCGATATTGGCCGCTGGCGGACACGATGC 3300  
Db 5912 AGCAGATCAAGGAAATCGAGCTTTCCTTGTTCGATATTGGCCGCTGGCGGACACGATGC 5853  
Qy 3301 GAGCGATGCCAAACGACACGCGCGCTCTGCGCTGTTCACACGCGCAACAGAAATCC 3360  
Db 5852 GAGCGATGCCAAACGACACGCGCGCTCTGCGCTGTTCACACGCGCAACAGAAATCC 5793  
Qy 3361 CGCGGAGGCGCTGCAAAACAAGGTCAATTTCCACGTCACAGGAGCTGAAGATCACCT 3420  
Db 5792 CGCGGAGGCGCTGCAAAACAAGGTCAATTTCCACGTCACAGGAGCTGAAGATCACCT 5733  
Qy 3421 ACACCGCGCTCGAGCTCGCGGCGCACGATACGAACTGGTGTGCGACGAGGTGTGGAGT 3480  
Db 5732 ACACCGCGCTCGAGCTCGCGGCGCACGATACGAACTGGTGTGCGACGAGGTGTGGAGT 5673  
Qy 3481 ACGGAAGCGGACCCCTATCGCGAGCGCGATCACCTTCAGTTTACGAGCTTTCGCAGG 3540  
Db 5672 ACGGAAGCGGACCCCTATCGCGAGCGCGATCACCTTCAGTTTACGAGCTTTCGCAGG 5613  
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Qy 3601 TACAGGCGAGCGGATGGGCTTTCAGTCCGACCGCGTTGGGCACCTTGAATTCGTTGTCG 3660  
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Qy 3661 TGCTGACCGGCTTCGCGCTCTGACCGGTGGCAAGAAAACTGCCGTTGCGAGTCTCTGA 3720  
Db 5492 TGCTGACCGGCTTCGCGCTCTGACCGGTGGCAAGAAAACTGCCGTTGCGAGTCTCTGA 5433  
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Db 5432 TCGACAGGAAATCGTCTGCTGTTTCTGCGACCACTACACGAAATTCATATGGGAGA 5373  
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Db 5312 AGCGGTAACCGCTCAAGCTGGAATCTTCGCCCTCATGTGGGATTCGATTCACCGCGG 5253  
Qy 3901 TGAAGAGTCGCGGACGAGTCGCGAGGCGCTCGAGAGTTCGAGGAGCGGCGCTGG 3960  
Db 5252 TGAAGAGTCGCGGACGAGTCGCGGAGGCGCTCGAGAGTTCGAGGAGCGGCGCTGG 5193  
Qy 3961 TGAAGACGCGCTGGGTCAATGATACCTGTGTGATTCGAAACGCTAGGGGCTTGTGGGGT 4020

Db 5192 TGGAAACACGCTGGGTCAATGATGACCTGCTGCAATTGCAAAACGCTTAGGCGCTTGTGGGGT 5133  
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RESULT 6  
US-08-992-801-1/c  
; Sequence 1, Application US/08992801  
; Patent No. 6107544  
; GENERAL INFORMATION:  
; APPLICANT: Ryals, John  
; APPLICANT: Uknes, Scott  
; APPLICANT: Ward, Eric  
; APPLICANT: Delaney, Terry  
; APPLICANT: Lawton, Ray  
; APPLICANT: Weymann, Kris  
; APPLICANT: Steiner, Henry-York  
; APPLICANT: Maleck, Klaus  
; TITLE OF INVENTION: Method For Breeding Disease Resistance  
; TITLE OF INVENTION: Into Plants  
; NUMBER OF SEQUENCES: 1  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: No. 6107544artis Corporation  
; STREET: 3054 Cornwallis Road  
; CITY: Research Triangle Park  
; STATE: NC  
; COUNTRY: USA  
; ZIP: 27709  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/992,801  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA: US 08/648,949  
; APPLICATION NUMBER:  
; FILING DATE: 16-MAY-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/165,248  
; FILING DATE: 10-DEC-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/002,285  
; FILING DATE: 08-JAN-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meigs, J. Timothy  
; REGISTRATION NUMBER: 38,241  
; REFERENCE/DOCKET NUMBER: CGC1673/CIP3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 919-541-8587  
; TELEFAX: 919-541-8689  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1413 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; DESCRIPTION: /desc = "PR-1/luc construct"  
; US-08-992-801-1  
Query Match 29.0%; Score 1393; DB 3; Length 14113;  
Best Local Similarity 98.6%; Pred. No. 0;  
Matches 1405; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

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Db 6512 CCATGGCTCCTCAAGAAAGAGCGACTTCGCGAGCTGCTGTTATTCGTCAGGGGCAAGATTTC 6453



QY 2701 GGAATACCAAGTACGAGAAAGGACGGCCAGACGGTCTCTACGGACCGACTTCATTGCGGATA 2760  
DB 6452 GGAATACCAAGTACGAGAAAGGACGGCCAGACGGTCTACGGACCGACTTCATTGCGGATA 6393  
QY 2761 AGGTGGATTATCTGGACACCAAGGACACCGAGCGGGTCAATCAGGAATAGGGCAATTG 2820  
DB 6392 AGGTGGATTATCTGGACACCAAGGACACCGAGCGGGTCAATCAGGAATAGGGCAATTG 6333  
QY 2821 CCCCGCGTGGTGGGCGCAATCCCGCAAGGAGGGTGAATGAATCGGACGCTTTGACCGGA 2880  
DB 6332 CCCCGCGTGGTGGGCGCAATCCCGCAAGGAGGGTGAATGAATCGGACGCTTTGACCGGA 6273  
QY 2881 AGGCATACAGGCAAGAACTGATCGACGCGGGTTTCGCGCGAGGATGCCGAAACCATCG 2940  
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QY 2941 CAAGCCGCAACCGTCATCGCGTGGCGCCCGCGAARACCTTCCAGTCCGTCGGTCGATGGTCC 3000  
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QY 3301 GAGCGATGCAACGACACGGCCCGCTTGCCTCTGTTCCACCGCGCAACAGAAATCC 3360  
DB 5852 GAGCGATGCAACGACACGGCCCGCTTGCCTCTGTTCCACCGCGCAACAGAAATCC 5793  
QY 3361 CGCGGAGGCGTGCACAAACAGGTCAATTTCCACGTCAACAGGACGTGAAGTACACCT 3420  
DB 5792 CGCGGAGGCGTGCACAAACAGGTCAATTTCCACGTCAACAGGACGTGAAGTACACCT 5733  
QY 3421 ACACCGGCGTGCAGCTGCGGGCGGACGATGACGAACTGGTGTGGCAGCAGGTTTGGAGT 3480  
DB 5732 ACACCGGCGTGCAGCTGCGGGCGGACGATGACGAACTGGTGTGGCAGCAGGTTTGGAGT 5673  
QY 3481 ACGGGAAGCGCACCTTATCGGGAGCGGATACCTTTCAGTTCTACGAGCTTTGCCAGG 3540  
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DB 5612 ACTGGGCTGGTGCATCAATGGCCGCTATTACACGAAGCGCGAGGAATCGTGTCCGCGC 5553  
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DB 5552 TACAGCGACGGCGATGGGCTTACGTCGCGACCGCGTTGGCACCTTGGAAATCGGTGTGC 5493  
QY 3661 TGTGTACCGCTTCCCGCTCTGGACCGGTGGGCAAGAAACGTCCTCCGTTGCCAGGTCCTGA 3720  
DB 5492 TGTGTACCGCTTCCCGCTCTGGACCGGTGGGCAAGAAACGTCCTCCGTTGCCAGGTCCTGA 5433  
QY 3721 TCGACCGAAGAAATCGTGTGCTGTTGCTGGGACCACTACACGAAATTCATATGGGAGA 3780  
DB 5432 TCGACCGAAGAAATCGTGTGCTGTTGCTGGGACCACTACACGAAATTCATATGGGAGA 5373  
QY 3781 AGTACCGCAAGCTGTGCGCGACGGGCCCGAGCGGATGTTTCGACTATTTCAGTCTGCACCGGG 3840

DB 5372 AGTACCGCAAGCTGTGCGCGACGGCCGACGGAGTGTTCGACTATTTCAGTCTGCACCGGG 5313  
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DB 5312 AGCCGTACCGCTCAAGCTGGAAACCTTCGGCTCATGTCCGATCGGATTCACCCGG 5253  
QY 3901 TGAAGAAGTGGCGCGACGAGCGGTGCGGAAAGCCCTGCGAAGAGTTGCGAGGCGCGGCTGG 3960  
DB 5252 TGAAGAAGTGGCGCGACGAGCGGTGCGGAAAGCCCTGCGAAGAGTTGCGAGGCGCGGCTGG 5193  
QY 3961 TGAACACACGCTGGGTCATATGATGACCTGCTGATTCGAAACCGCTAGGGCTTTGTGGGT 4020  
DB 5192 TGAACACACGCTGGGTCATATGATGACCTGCTGATTCGAAACCGCTAGGGCTTTGTGGGT 5133  
QY 4021 CAGTTCCGCTGGGGTTTCAGCAGCGCGCTTTACTGGCATTTTC 4065  
DB 5132 CAGTTCCGCTGGGGTTTCAGCAGCGCGCTTTACTGGCATTTTC 5088

## RESULT 7

US-09-223-535-1/c  
; Sequence 1, Application US/09223535  
; Patent No. 6232525  
; GENERAL INFORMATION:  
; APPLICANT: Ryals, John  
; APPLICANT: Uknes, Scott  
; APPLICANT: Ward, Eric  
; APPLICANT: Delaney, Terry  
; APPLICANT: Lawton, Kay  
; APPLICANT: Weymann, Kris  
; APPLICANT: Steiner, Henry-York  
; APPLICANT: Maleck, Klaus  
; TITLE OF INVENTION: Method For Breeding Disease Resistance  
; TITLE OF INVENTION: Into Plants  
; NUMBER OF SEQUENCES: 1  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: No. 6232525artis Corporation  
; STREET: 3054 Cornwallis Road  
; CITY: Research Triangle Park  
; STATE: NC  
; COUNTRY: USA  
; ZIP: 27709  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/223,535  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/992,801  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/165,248  
; FILING DATE: 10-DEC-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/002,285  
; FILING DATE: 08-JAN-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meigs, J. Timothy  
; REGISTRATION NUMBER: 38,241  
; REFERENCE/DOCKET NUMBER: CGC1673/CIP3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 919-541-8587  
; TELEFAX: 919-541-8689  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1413 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single

; TOPOLOGY: linear		Query Match		29.0%; Score 1393; DB 3; Length 14113;	
; MOLECULE TYPE: other nucleic acid		Best Local Similarity		98.6%; Pred. No. 0;	
; DESCRIPTION: /desc = "PR-1/luc construct"		Matches 1405; Conservative		0; Mismatches 20; Indels 0; Gaps 0;	
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QY	2701	GGAAATACCAAGTACGAGACGGCCAGACGGTCTACGGGACCGACTTCATTGCCGATA	2760		
DB	6452	GGAAATACCAAGTACGAGACGGCCAGACGGTCTACGGGACCGACTTCATTGCCGATA	6393		
QY	2761	AGGTGATTTATCTGGACACCAAGGCACAGGGCGGTCAAAATCAGGAATAAGGGCACATTG	2820		
DB	6392	AGGTGATTTATCTGNACACCAAGGCACAGGGCGGTCAAAATCAGGAATAAGGGCACATTG	6333		
QY	2821	CCCCGGCTGAGTCGGGGCAATCCCGCAAGGAGGTGAATGAATCGAACCTTTGACCGGA	2880		
DB	6332	CCCCGGCTGAGTCGGGGCAATCCCGCAAGGAGGTGAATGAATCGAACCTTTGACCGGA	6273		
QY	2881	AGGCATACAGCAAGAACTGATCGACGCGGGTTTTCCGCGAGGATGCCGNAACCATCG	2940		
DB	6272	AGGCATACAGCAAGAACTGATCGACGCGGGTTTTCCGCGAGGATGCCGNAACCATCG	6213		
QY	2941	CAAGCCGACCGTTCATCGCTGCGCCCGCGAAACCTTCCAGTCCGTCCGGTCCGATGGTCC	3000		
DB	6212	CAAGCCGACCGTTCATCGCTGCGCCCGCGAAACCTTCCAGTCCGTCCGGTCCGATGGTCC	6153		
QY	3001	AGCAAGCTACGGCCCAAGATCGAGCGCACAGCGGTGCAACTGGCTCCCTCGCCCTGGCCG	3060		
DB	6152	AGCAAGCTACGGCCCAAGATCGAGCGCACAGCGGTGCAACTGGCTCCCTCGCCCTGGCCG	6093		
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DB	5912	AGCAGATCAAGGAATACGAGTTTCCCTGTTTCGATATTGGCCGTGGCGGACACGATGC	5853		
QY	3301	GAGCGATGCCAAACGACACGCGCCGCTCTGCCCTGTTTACACGCGCAACAAAGAAATCC	3360		
DB	5852	GAGCGATGCCAAACGACACGCGCCGCTCTGCCCTGTTTACACGCGCAACAAAGAAATCC	5793		
QY	3361	CGCGCAGGCGCTGCCAAACAAAGTCAATTTTCCAGTCAACAAAGGACGTGAAGATCACT	3420		
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QY	3421	ACACCGCGTTCGAGCTGGGGCGACGATGACGAACTGGTGTGGCAGCAGGTGTGGAGT	3480		
DB	5732	ACACCGCGTTCGAGCTGGGGCGACGATGACGAACTGGTGTGGCAGCAGGTGTGGAGT	5673		
QY	3481	ACGGAAGCGCACCCCTATCGGCGAGCGGATCACCTTTCAGCTTCTACGAGCTTTGCCAGG	3540		
DB	5672	ACGGAAGCGCACCCCTATCGGCGAGCGGATCACCTTTCAGCTTCTACGAGCTTTGCCAGG	5613		
QY	3541	ACCTGGGCTGGTTCGATCAATGGCCGGTATTACACGAAGGCGGAGGAATGCTGTGCGGCC	3600		
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RESULT 8				
US-09-185-244-8				
; Sequence 8, Application US/09185244				
; Patent No. 6333449				
; GENERAL INFORMATION:				
; APPLICANT: MICHAELS, Frank				
; APPLICANT: JOHNSON, Kirk				
; TITLE OF INVENTION: GLUFOSINATE TOLERANT RICE				
; FILE REFERENCE: 514412-2001				
; CURRENT APPLICATION NUMBER: US/09/185,244				
; CURRENT FILING DATE: 1998-11-03				
; NUMBER OF SEQ ID NOS: 9				
; SOFTWARE: PatentIn Ver. 2.1				
; SEQ ID NO 8				
; LENGTH: 4161				
; TYPE: DNA				
; ORGANISM: Artificial Sequence				
; FEATURE:				
; OTHER INFORMATION: Description of Artificial Sequence: plasmid				
; OTHER INFORMATION: pBS/35Sbar				
US-09-185-244-8				
Query Match	21.3%;	Score 1025.2;	DB 4;	Length 4161;
Best Local Similarity	99.2%;	Pred. No. 2.6e-291;		
Matches 1030;	Conservative	0;	Mismatches 8;	Indels 0; Gaps 0;
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QY	1655	CTGGTATTAAAGTTTTAGAAATGCAAGGAAACAGTGAATTGGAGTTCTGTGTATAATT	1714	
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Db 301 AAAATGACGGACAGCCGGTATAAAGGACACCATATGATGTGAAACGGGAAAAAGGACATG 360  
QY 1955 ATGCTATGCTGGAAGGAAGCTCCCTGTTCCAAAGGTCCTGCACATTTGAAACGGCATGAT 2014  
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Db 481 GATGAACAAAGCCCTGAAAGATTATCGAGCTGTATGCGGAGTGCAATCAGGCTCTTTTAC 540  
QY 2135 TCCATCGACATATCGGATTCCTCTATACGAATAGCTTAGACAGCCGCTTAGCCGAATTG 2194  
Db 541 TCCATCGACATATCGGATTCCTCTATACGAATAGCTTAGACAGCCGCTTAGCCGAATTG 600  
QY 2195 GATTACTTACTGAATAACGATCTGGCCGATGTGATTTTAAAGACGGAAAGCCCGAAGACACT 2254  
Db 601 GATTACTTACTGAATAACGATCTGGCCGATGTGATTTTAAAGACGGAAAGCCCGAAGACACT 660  
QY 2255 CCATTTAAAGATCCGCGAGCTGTATGATTTTAAAGACGGAAAGCCCGAAGACACT 2314  
Db 661 CCATTTAAAGATCCGCGAGCTGTATGATTTTAAAGACGGAAAGCCCGAAGACACT 720  
QY 2315 CTGTCTTTCCACGGACCTGGGAGACAGCAACATCTTTGTGAAAGATGCGCAAGTA 2374  
Db 721 CTGTCTTTTCCACGGACCTGGGAGACAGCAACATCTTTGTGAAAGATGCGCAAGTA 780  
QY 2375 AGTGGCTTTATTGATCTTGGGAGAACGGCAGGCGGACAGTGGTATGACATTTGCTTTC 2434  
Db 781 AGTGGCTTTATTGATCTTGGGAGAACGGCAGGCGGACAGTGGTATGACATTTGCTTTC 840  
QY 2435 TGGCTCCGGTTCGATCAGGGAGGATATCGGGGAAAGAACAGTATGTCAGGCTATTTTGTAC 2494  
Db 841 TGGCTCCGGTTCGATCAGGGAGGATATCGGGGAAAGAACAGTATGTCAGGCTATTTTGTAC 900  
QY 2495 TTTACTGGGATCAAGCTGATTTGGGAGAAAATAAAATATATATTTTACTGGATGAATTG 2554  
Db 901 TTTACTGGGATCAAGCTGATTTGGGAGAAAATAAAATATATATTTTACTGGATGAATTG 960  
QY 2555 TTTTGTACCTAGATGTGGCGCAACGATGCGCGGACAGGAGGCGGACCGACTTCTT 2614  
Db 961 TTTTGTACCTAGATGTGGCGCAACGATGCGCGGACAGGAGGCGGACCGACTTCTT 1020  
QY 2615 CCGCATCAAGTGTTTTGG 2632  
Db 1021 CCGCAAAAGGATCTAGG 1038

RESULT 9

US-09-471-913-1  
; Sequence 1, Application US/09471913  
; Patent No. 6468747  
; GENERAL INFORMATION:  
; APPLICANT: De Beuckeleer, et al  
; TITLE OF INVENTION: Glufosinate Tolerant Rice  
; FILE REFERENCE: 514412-2003  
; CURRENT APPLICATION NUMBER: US/09/471, 913  
; CURRENT FILING DATE: 1999-12-23  
; PRIOR APPLICATION NUMBER: 09/185,143  
; PRIOR FILING DATE: 1998-11-03  
; PRIOR APPLICATION NUMBER: 09/185,244  
; PRIOR FILING DATE: 1998-11-03

Query Match 21.3%; Score 1025.2; DB 4; Length 4161;  
Best Local Similarity 99.2%; Pred. No. 2.6e-291;  
Matches 1030; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
QY 1595 CGSCTCCGTCGATACCTATGTCACGCCAACCTTTGAAAAACACTTTGAAAAACACTTTGAAAAACACTTTG 1654  
Db 1 CGSCTCCGTCGATACCTATGTCACGCCAACCTTTGAAAAACACTTTGAAAAACACTTTGAAAAACACTTTG 60  
QY 1655 CTGGTATTTAAGGTTTTAGAAATGCAAGGAACAGTGAATTTGGAGTTCGCTTGTATAAAT 1714  
Db 61 CTGGTATTTAAGGTTTTAGAAATGCAAGGAACAGTGAATTTGGAGTTCGCTTGTATAAAT 120  
QY 1715 AGCTTCTGGGTATCTTTTAAATACCTGTAGAAAAAGGAAGAAATAATAAATGGCTAAA 1774  
Db 121 AGCTTCTGGGTATCTTTTAAATACCTGTAGAAAAAGGAAGAAATAATAAATGGCTAAA 180  
QY 1775 ATGAGAAATACCCGGAATTTGAAAAACCTGCGAAAAATACCGCTGCGTAAAAAGATACG 1834  
Db 181 ATGAGAAATACCCGGAATTTGAAAAACCTGCGAAAAATACCGCTGCGTAAAAAGATACG 240  
QY 1835 GAAGGAATCTCTCTGCTAAGGTATATAAGCTGGTGGGAGAAAAATGAAAAACCTATATTTA 1894  
Db 241 GAAGGAATCTCTCTGCTAAGGTATATAAGCTGGTGGGAGAAAAATGAAAAACCTATATTTA 300  
QY 1895 AAAATGACGGACAGCCGGTATAAAGGACCACTATGATGTGAAACGGGAAAAAGGACATG 1954  
Db 301 AAAATGACGGACAGCCGGTATAAAGGACCACTATGATGTGAAACGGGAAAAAGGACATG 360  
QY 1955 ATGCTATGCTGGAAGGAAGCTGCTGTTCCAAAGGTCCTGCACATTTTCAACGGCATGAT 2014  
Db 361 ATGCTATGCTGGAAGGAAGCTGCTGTTCCAAAGGTCCTGCACATTTTCAACGGCATGAT 420  
QY 2015 GGCTGGAGCAATCTGCTCATGAGTGAGGCCGATGGCGTCTTTGCTCGGAAGAGTATGAA 2074

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Db 421 GGCTGGAGCAATCTGCTCATGTTGTGAGCCGATGGCGTCTTCTGCTCGGAAGATGAA 480
Qy 2075 GATGAACAAAGCCCTGAAAGATTTATCGAGCTGTATCGGAGTGCATCAGGCTCTTTTCAC 2134
Db 481 GATGAACAAAGCCCTGAAAGATTTATCGAGCTGTATCGGAGTGCATCAGGCTCTTTTCAC 540
Qy 2135 TCCATCGACATATCGGATTTGCTCCCTATACGAATAGCTTAGCAGCCGCTTAGCGGAATTG 2194
Db 541 TCCATCGACATATCGGATTTGCTCCCTATACGAATAGCTTAGCAGCCGCTTAGCGGAATTG 600
Qy 2195 GATTACTTACTGAATAACGATCTGGCCGATGTGATTTGCGAAACTGGGAAGAAGACACT 2254
Db 601 GATTACTTACTGAATAACGATCTGGCCGATGTGATTTGCGAAACTGGGAAGAAGACACT 660
Qy 2255 CCATTTAAAGATCCGCGAGCTGTATGATTTTTTAAAGACGGAAGAACCCGGAAGAGAA 2314
Db 661 CCATTTAAAGATCCGCGAGCTGTATGATTTTTTAAAGACGGAAGAACCCGGAAGAGAA 720
Qy 2315 CTGTCTTTTCCACCGGACCTGGGAGACGCAACATCTTCTGGAAGATGGCAAGTA 2374
Db 721 CTGTCTTTTCCACCGGACCTGGGAGACGCAACATCTTCTGGAAGATGGCAAGTA 780
Qy 2375 AGTGGCTTTTATGATCTTGGGAGAAAGCGGAGCGGCAAGTGTATGACATTTGCCCTTC 2434
Db 781 AGTGGCTTTTATGATCTTGGGAGAAAGCGGAGCGGCAAGTGTATGACATTTGCCCTTC 840
Qy 2435 TGGCTCCGCTCGATCAGGAGGATATCGGGAAGAAACAGTATGTCGAGCTATTTTTTGAC 2494
Db 841 TGGCTCCGCTCGATCAGGAGGATATCGGGAAGAAACAGTATGTCGAGCTATTTTTTGAC 900
Qy 2495 TTACTGGGGATCAAGCTGATGGGAGAAATATAATATTTTACTGGATGAATTG 2554
Db 901 TTACTGGGGATCAAGCTGATGGGAGAAATATAATATTTTACTGGATGAATTG 960
Qy 2555 TTTTAGTACCTAGATGCGGCAACGATGCGGCGCAAGCAGGAGCGCACCGACTTCTT 2614
Db 961 TTTTAGTACCTAGATGCGGCAACGATGCGGCGCAAGCAGGAGCGCACCGACTTCTT 1020
Qy 2615 CCGCATCAAGTGTGTTGG 2632
Db 1021 CCGCAAAAGGATCTAGG 1038
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## RESULT 10

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US-09-171-517B-15
; Sequence 15, Application US/09171517B
; Patent No. 6355254
; GENERAL INFORMATION:
; APPLICANT: Finlay, B. Brett
; APPLICANT: Kenny, Brendan
; APPLICANT: Stein, Markus
; TITLE OF INVENTION: PATHOGENIC ESCHERICHIA COLI ASSOCIATED PROTEIN
; FILE REFERENCE: 07422/019001
; CURRENT APPLICATION NUMBER: US/09/171,517B
; CURRENT FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: PCT/CA97/00265
; PRIOR FILING DATE: 1997-04-23
; PRIOR APPLICATION NUMBER: 60/015,999
; PRIOR FILING DATE: 1996-04-23
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 856
; TYPE: DNA
; ORGANISM: Escherichia coli
US-09-171-517B-15
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Query Match 16.8%; Score 807; DB 4; Length 856;
Best Local Similarity 99.4%; Pred. No. 1.9e-227;
Matches 810; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 1756 GAAATAATAATGCTAAATGAGATATATCACCGGAATTGAAAAAATGATCGAAAAATA 1815
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Db 26 GGAGGAATAAATGGCTAAAATGAGATAATCACCGGAATTTGAAAAAACTGATCGAAAAATA 85
Qy 1816 CCGCTCGCTAAAAGATACGGAAGGATGCTCTCTGCTAAGGTATATAAGCTGTTGGGAGA 1875
Db 86 CCGCTCGCTAAAAGATACGGAAGGATGCTCTCTGCTAAGGTATATAAGCTGTTGGGAGA 145
Qy 1876 AAATGAAAAACCTATATTTTAAAAATGACGACAGCCGATATAAAGGACACCACTTATGATG 1935
Db 146 AAATGAAAAACCTATATTTTAAAAATGACGACAGCCGATATAAAGGACACCACTTATGATG 205
Qy 1936 GGAACCGGAAAAAGGACATGATGCTATGGCTGGAAGAAAAGCTGCTGTTTCCAAAGTCTCT 1995
Db 206 GGAACCGGAAAAAGGACATGATGCTATGGCTGGAAGAAAAGCTGCTGTTTCCAAAGTCTCT 265
Qy 1996 GCATTTTGAACGGCATGATGGCTGGAGCAATCTGCTCATGAGTGAGCGCGATGGCGTCTCT 2055
Db 266 GCATTTTGAACGGCATGATGGCTGGAGCAATCTGCTCATGAGTGAGCGCGATGGCGTCTCT 325
Qy 2056 TTGCTCGGAAGAGTATGAAGATGAACAAAGCCCTGAAAAAGATTATCCAGCTGTATCGGA 2115
Db 326 TTGCTCGGAAGAGTATGAAGATGAACAAAGCCCTGAAAAAGATTATCCAGCTGTATCGGA 385
Qy 2116 GTGCATCAGGCTCTTTTCACTCCATCGACATATCGGATTTGTCCTATACGAATAGCTTAGA 2175
Db 386 GTGCATCAGGCTCTTTTCACTCCATCGACATATCGGATTTGTCCTATACGAATAGCTTAGA 445
Qy 2176 CAGCCCTTAGCGGAATTTGATTTACTTAATAACGATCTGGCCGATGTTGGATTGCGGA 2235
Db 446 CAGCCCTTAGCGGAATTTGATTTACTTAATAACGATCTGGCCGATGTTGGATTGCGGA 505
Qy 2236 AAATCGGGAAGAGACACTCCATTTTAAAGATCCGCGCGAGCTGTATGATTTTAAAGAC 2295
Db 506 AAATCGGGAAGAGACACTCCATTTTAAAGATCCGCGCGAGCTGTATGATTTTAAAGAC 565
Qy 2296 GGAAGAGCCGGAAGAGAACTTGTCTTTTCCACGGCGACTGGGAGACAGCAACATCTT 2355
Db 566 GGAAGAGCCGGAAGAGAACTTGTCTTTTCCACGGCGACTGGGAGACAGCAACATCTT 625
Qy 2356 TGTGAAAGATGGCAAAAGTAAAGTGGCTTTTATGATCTTGGAGAGAGCGGCGGAGCAA 2415
Db 626 TGTGAAAGATGGCAAAAGTAAAGTGGCTTTTATGATCTTGGAGAGAGCGGCGGAGCAA 685
Qy 2416 GTGATATGACATTTGCTTCTGCGTCCGATCAGGAGGATATCGGGGAAGAACAGTA 2475
Db 686 GTGATATGACATTTGCTTCTGCGTCCGATCAGGAGGATATCGGGGAAGAACAGTA 745
Qy 2476 TGTGAGCTATTTTTTGTACTTACTGGGATCAAGCTGATTTGGGAAAAATAAAATATTA 2535
Db 746 TGTGAGCTATTTTTTGTACTTACTGGGATCAAGCTGATTTGGGAAAAATAAAATATTA 805
Qy 2536 TATTTTACTGGATGAATTTGTTTAGTACCTAGATG 2570
Db 806 TATTTTACTGGATGAATTTGTTTAGTACCTGGAGG 840
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## RESULT 11

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US-09-134-000C-3304
; Sequence 3304, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3304
; LENGTH: 795
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; TYPE: DNA
; ORGANISM: Enterococcus faecalis
; US-09-134-000C-3304

Query Match      16.5%; Score 795; DB 4; Length 795;
Best Local Similarity 100.0%; Pred. No. 6.2e-224; Mismatches 0; Indels 0; Gaps 0;
Matches 795; Conservative 0;

QY 1766 ATGGCTAAATGAGATATCACCGGAATTGAAAAAACTGATCGAAAAATACCGCTCGGTA 1825
DB 1 ATGGCTAAATGAGATATCACCGGAATTGAAAAAACTGATCGAAAAATACCGCTCGGTA 60

QY 1826 AAAGATACGGAAGAAATGCTCTCTGTAAGGTATATAAGCTGTGGGAGAAAAATGAAAAAC 1885
DB 61 AAAGATACGGAAGAAATGCTCTCTGTAAGGTATATAAGCTGTGGGAGAAAAATGAAAAAC 120

QY 1886 CTATATTTAAAAATGACGACACCGGTATAAAGGACCACTATGATGTGGAAACGGGA 1945
DB 121 CTATATTTAAAAATGACGACACCGGTATAAAGGACCACTATGATGTGGAAACGGGA 180

QY 1946 AAGGACATGATGCTATGGCTGGAAGAAAGCTGCTGTTCCAAAGGTCTCTGCACTTTGAA 2005
DB 181 AAGGACATGATGCTATGGCTGGAAGAAAGCTGCTGTTCCAAAGGTCTCTGCACTTTGAA 240

QY 2006 CGGCATGATGGCTGGAGCAATCTGCTCATGAGTGAGCGCGATGGCGTCTTTGCTCGGAA 2065
DB 241 CGGCATGATGGCTGGAGCAATCTGCTCATGAGTGAGCGCGATGGCGTCTTTGCTCGGAA 300

QY 2066 GAGTATGAAGTAAAGCAAAAGCCCTGAAAGATTTATCGAGCTGTATGGGAGTGCATCAGG 2125
DB 301 GAGTATGAAGTAAAGCAAAAGCCCTGAAAGATTTATCGAGCTGTATGGGAGTGCATCAGG 360

QY 2126 CTCTTTCACTCCATCGACATATCGGATTTGCCCTATACGAATAGCTTTAGACAGCCGCTTA 2185
DB 361 CTCTTTCACTCCATCGACATATCGGATTTGCCCTATACGAATAGCTTTAGACAGCCGCTTA 420

QY 2186 GCCGAATTGGATTTACTTGAATAACGATCTGGCCGATGTGGATTTGCCGAATCTGGAA 2245
DB 421 GCCGAATTGGATTTACTTGAATAACGATCTGGCCGATGTGGATTTGCCGAATCTGGAA 480

QY 2246 GAAGACATCCATTTAAAGATCCGCGGAGCTGTATGATTTTAAAGACGGAAGAGCCC 2305
DB 481 GAAGACATCCATTTAAAGATCCGCGGAGCTGTATGATTTTAAAGACGGAAGAGCCC 540

QY 2306 GAAGAGGAATCTGCTTTTCCACGCGGACCTGGGAGACAGCAACATCTTTGTGAAGAT 2365
DB 541 GAAGAGGAATCTGCTTTTCCACGCGGACCTGGGAGACAGCAACATCTTTGTGAAGAT 600

QY 2366 GGCAAAATGATGGCTTTTATTTGATCTTGGGAGAAAGCGGACGAGGCGCAAGTGGTATGAC 2425
DB 601 GGCAAAATGATGGCTTTTATTTGATCTTGGGAGAAAGCGGACGAGGCGCAAGTGGTATGAC 660

QY 2426 ATTGCTTTCTGCTCGGTCGATCAGGAGGATATCGGGAGAAACAGATATGTCGAGCTA 2485
DB 661 ATTGCTTTCTGCTCGGTCGATCAGGAGGATATCGGGAGAAACAGATATGTCGAGCTA 720

QY 2486 TTTTGTGACTTACTGGGGTCAAGCTGTATGGGAGAAATATAATATTTATTTTACTG 2545
DB 721 TTTTGTGACTTACTGGGGTCAAGCTGTATGGGAGAAATATAATATTTATTTTACTG 780

QY 2546 GATGAATTTGTTAG 2560
DB 781 GATGAATTTGTTAG 795
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RESULT 12  
US-09-280-428A-11  
; Sequence 11, Application US/09280428A  
; Patent No. 6495738  
; GENERAL INFORMATION:  
; APPLICANT: Folkerts, Otto  
; APPLICANT: Merlo, Donald J  
; TITLE OF INVENTION: Modification of Fatty Acid Composition in Plants by

```
; TITLE OF INVENTION: Expression of A Fungal Acyl-CoA Desaturase
; FILE REFERENCE: 50612
; CURRENT APPLICATION NUMBER: US/09/280,428A
; CURRENT FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: 60/079840
; PRIOR FILING DATE: 1998-03-30
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 10323
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:pDAB1542
; US-09-280-428A-11
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Query Match      12.9%; Score 618.6; DB 4; Length 10323;
Best Local Similarity 99.4%; Pred. No. 4.4e-171;
Matches 621; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CCGGGCTGCTTGCCCTCGCCGCTGGGCTGGCGCCGCTCTATGGCCCTGCAAAACGCGCCAG 60
DB 9628 CCGGGCTGCTTGCCCTCGCCGCTGGGCTGGCGCCGCTCTATGGCCCTGCAAAACGCGCCAG 9687

QY 61 AAACGCCGTCGAAGCCGTCGTGCGAGACACCGCGGCGCGCGGCTTGTGATACCTCGCGG 120
DB 9688 AAACGCCGTCGAAGCCGTCGTGCGAGACACCGCGGCGCGCGGCTTGTGATACCTCGCGG 9747

QY 121 AAAACTTGGCCCTCACTGACAGATGAGGGCGGAGCGTTGACACTTGAGGGGCGGACTCAC 180
DB 9748 AAAACTTGGCCCTCACTGACAGATGAGGGCGGAGCGTTGACACTTGAGGGGCGGACTCAC 9807

QY 181 CCGGCGCGCGCTTGACAGATGAGGGCGAGGCTCGATTTTCGCGCGGCGACGCTGAGCTGGC 240
DB 9808 CCGGCGCGCGCTTGACAGATGAGGGCGAGGCTCGATTTTCGCGCGGCGACGCTGAGCTGGC 9867

QY 241 CAGCCTCGCAAAATCGCGCAAAAACGCGCTGATTTTACGCGAGTTTCCACAGATGATGTGA 300
DB 9868 CAGCCTCGCAAAATCGCGCAAAAACGCGCTGATTTTACGCGAGTTTCCACAGATGATGTGA 9927

QY 301 CAAAGCTCGGGATAGTGCCTCGGCTATGACACTTGAGGGGCGGACTACTGACAGAT 360
DB 9928 CAAAGCTCGGGATAGTGCCTCGGCTATGACACTTGAGGGGCGGACTACTGACAGAT 9987

QY 361 GAGGGCGCGATCTCTTGACACTTTGAGGGCGAGAGTCTGACAGATGAGGGGCGCACCTAT 420
DB 9988 GAGGGCGCGATCTCTTGACACTTTGAGGGCGAGAGTCTGACAGATGAGGGGCGCACCTAT 10047

QY 421 TGACATTTGAGGGGCTGTCCACAGGACAGAAAAATCCAGCATTTTGCAAGGGTTTCCGCGCGT 480
DB 10048 TGACATTTGAGGGGCTGTCCACAGGACAGAAAAATCCAGCATTTTGCAAGGGTTTCCGCGCGT 10107

QY 481 TTTTGGCCACCGCTAACCTGTCTTTTAACCTGCTTTTAAACCAATATTTATAAACCTTG 540
DB 10108 TTTTGGCCACCGCTAACCTGTCTTTTAACCTGCTTTTAAACCAATATTTATAAACCTTG 10167

QY 541 TTTTAAACAGGCTGCGCCCTGTGCGCTGACCGGCGACCGCGAAGGGGGTGCCCCC 600
DB 10168 TTTTAAACAGGCTGCGCCCTGTGCGCTGACCGGCGACCGCGAAGGGGGTGCCCCC 10227

QY 601 CTTCTCGAAACCTCCCGGAAAGGTA 625
DB 10228 CTTCTCGAAACCTCCCGGCGCGCTA 10252
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RESULT 13  
US-09-223-134-1  
; Sequence 1, Application US/09223134  
; Patent No. 6057490  
; GENERAL INFORMATION:  
; APPLICANT: Ryals, John  
; APPLICANT: Uknes, Scott  
; APPLICANT: Ward, Eric

```
/ APPLICANT: Delaney, Terry
/ APPLICANT: Lawton, Kay
/ APPLICANT: Weymann, Kris
/ APPLICANT: Steiner, Henry-York
/ APPLICANT: Maleck, Klaus
/ TITLE OF INVENTION: Method For Breeding Disease Resistance
/ TITLE OF INVENTION: Into Plants
/ NUMBER OF SEQUENCES: 1
/ CORRESPONDENCE ADDRESS:
/ ADDRESS: No. 6057490artis Corporation
/ STREET: 3054 Cornwallis Road
/ CITY: Research Triangle Park
/ STATE: NC
/ COUNTRY: USA
/ ZIP: 27709
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/223,134
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/992,801
/ FILING DATE:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/165,248
/ FILING DATE: 10-DEC-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/002,285
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Meigs, J. Timothy
/ REGISTRATION NUMBER: 38,241
/ REFERENCE/DOCKET NUMBER: CGC1673/CIP3
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 919-541-8587
/ TELEFAX: 919-541-8689
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1413 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: other nucleic acid
/ DESCRIPTION: /desc = "PR-1/luc construct"
/
/ US-09-223-134-1
/
/ Query Match 12.9%; Score 618.6; DB 3; Length 14113;
/ Best Local Similarity 99.4%; Pred. No. 5.5e-171;
/ Matches 621; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
/
/ QY 1 CCGGCTGTGGTCCCTCGCGCTGGCTGGCGGCGGCTATGGCCCTGCACACCGGCAG 60
/ DB 864 CCGGCTGTGGTCCCTCGCGCTGGCTGGCGGCGGCTATGGCCCTGCACACCGGCAG 923
/
/ QY 61 AAACGCGCTGAAGCCGTGTCGAGACACCGCGCGCGGCTGTGGATACCTCGCGG 120
/ DB 924 AAACGCGCTGAAGCCGTGTCGAGACACCGCGCGCGGCTGTGGATACCTCGCGG 983
/
/ QY 121 AAAATTGGCCCTCACTGACAGATGAGGGCGGCGGCTTGACACTTGAGGGGCGCACTCAC 180
/ DB 984 AAAATTGGCCCTCACTGACAGATGAGGGCGGCGGCTTGACACTTGAGGGGCGCACTCAC 1043
/
/ QY 181 CCGCGCGGCGGCTTGAAGATGAGGGCGGCGGCTTCGATTCGCGCGCGGCGGAGCTGGC 240
/ DB 1044 CCGCGCGGCGGCTTGAAGATGAGGGCGGCGGCTTCGATTCGCGCGCGGCGGAGCTGGC 1103
/
/ QY 241 CAGCCTCGAAATCGGCGGAAACCGCTGATTTTACGCGAGTTTCCACAGATGATGTGA 300
/ DB 1104 CAGCCTCGAAATCGGCGGAAACCGCTGATTTTACGCGAGTTTCCACAGATGATGTGA 1163
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QY 301 CAAGCCTGGGATAAGTGCCTGCGGTATTGACACTTGAGGGGCGCGCACTACTGACAGAT 360
DB 1164 CAAGCCTGGGATAAGTGCCTGCGGTATTGACACTTGAGGGGCGCGCACTACTGACAGAT 1223
QY 361 GAGGGGCGCGATCCTTTGACACTTGAGGGGCGAGAGTGCTGACAGATGAGGGGCGCACTAT 420
DB 1224 GAGGGGCGCGATCCTTTGACACTTGAGGGGCGAGAGTGCTGACAGATGAGGGGCGCACTAT 1283
QY 421 TGACATTTGAGGGGCTGTCCACAGGCGAGAAAATCCAGCAATTTTCAAGGGGTTTCCGCGCGT 480
DB 1284 TGACATTTGAGGGGCTGTCCACAGGCGAGAAAATCCAGCAATTTTCAAGGGGTTTCCGCGCGT 1343
QY 481 TTTTCGCGCACCGCTAACTGCTTTTAACTGCTTTTAAACCAATATTATATAACCTTG 540
DB 1344 TTTTCGCGCACCGCTAACTGCTTTTAACTGCTTTTAAACCAATATTATATAACCTTG 1403
QY 541 TTTTAAACAGGGCTGCGCCCTGTGCGCGTGACCGCGCACCGCGAGAGGGGGTGCCTCCC 600
DB 1404 TTTTAAACAGGGCTGCGCCCTGTGCGCGTGACCGCGCACCGCGAGAGGGGGTGCCTCCC 1463
QY 601 CTTCTCGAAACCTTCCCGGAAAGGTA 625
DB 1464 CTTCTCGAAACCTTCCCGGCGCGCTA 1488
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/ RESULT 14
/ US-08-992-801-1
/ Sequence 1, Application US/08992801
/ Patent No. 6107544
/ GENERAL INFORMATION:
/ APPLICANT: Ryals, John
/ APPLICANT: Uknes, Scott
/ APPLICANT: Ward, Eric
/ APPLICANT: Delaney, Terry
/ APPLICANT: Lawton, Kay
/ APPLICANT: Weymann, Kris
/ APPLICANT: Steiner, Henry-York
/ APPLICANT: Maleck, Klaus
/ TITLE OF INVENTION: Method For Breeding Disease Resistance
/ TITLE OF INVENTION: Into Plants
/ NUMBER OF SEQUENCES: 1
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: No. 6107544artis Corporation
/ STREET: 3054 Cornwallis Road
/ CITY: Research Triangle Park
/ STATE: NC
/ COUNTRY: USA
/ ZIP: 27709
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/992,801
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/648,949
/ FILING DATE: 16-MAY-1996
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/165,248
/ FILING DATE: 10-DEC-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/002,285
/ FILING DATE: 08-JAN-1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Meigs, J. Timothy
/ REGISTRATION NUMBER: 38,241
/ REFERENCE/DOCKET NUMBER: CGC1673/CIP3
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 919-541-8587
```



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; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14113 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "PR-1/luc construct"
; US-08-992-801-1

Query Match 12.9%; Score 618.6; DB 3; Length 14113;
Best Local Similarity 99.4%; Pred. No. 5.5e-171;
Matches 621; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CCGGGCTGGTTGCCCTCGCGCTGGCGCTGGCGCGCGCTGATGCGCCCTGCAAAAGCGCCGAG 60
DB 864 CCGGGCTGGTTGCCCTCGCGCTGGCGCTGGCGCGCGCTGATGCGCCCTGCAAAAGCGCCGAG 923

QY 61 AAACGCGCTGGAAGCGCTGTGCGAGACACCGCGCGCGCGCTGATGCGCCCTGCAAAAGCGCCGAG 120
DB 924 AAACGCGCTGGAAGCGCTGTGCGAGACACCGCGCGCGCGCTGATGCGCCCTGCAAAAGCGCCGAG 983

QY 121 AAAAATTGGCCCTCACTGACAGATGAGGGCGGAGCTTGACACTTGAAGGGCGGAGCTAC 180
DB 984 AAAAATTGGCCCTCACTGACAGATGAGGGCGGAGCTTGACACTTGAAGGGCGGAGCTAC 1043

QY 181 CCGGCGCGCTGTGACAGATGAGGGCGGAGCTTGACACTTGAAGGGCGGAGCTAC 240
DB 1044 CCGGCGCGCTGTGACAGATGAGGGCGGAGCTTGACACTTGAAGGGCGGAGCTAC 1103

QY 241 CAGCCTCGCAAAATCGCGGAAACCGCTGATTTACCGAGTTTCCACAGATGATGTGA 300
DB 1104 CAGCCTCGCAAAATCGCGGAAACCGCTGATTTACCGAGTTTCCACAGATGATGTGA 1163

QY 301 CAAAGCTGGGATAGTGCCTCGCGCTGATTTGACACTTGAAGGGCGGAGCTAC 360
DB 1164 CAAAGCTGGGATAGTGCCTCGCGCTGATTTGACACTTGAAGGGCGGAGCTAC 1223

QY 361 GAGGGCGCGATCTTTGACACTTTAGGGCGAGTCTGACAGATGAGGGCGGAGCTAC 420
DB 1224 GAGGGCGCGATCTTTGACACTTTAGGGCGAGTCTGACAGATGAGGGCGGAGCTAC 1283

QY 421 TGACATTTGAGGGCTGTCCACAGGCGAGAAATCCAGCATTTGCAAGGTTTCCGCGCT 480
DB 1284 TGACATTTGAGGGCTGTCCACAGGCGAGAAATCCAGCATTTGCAAGGTTTCCGCGCT 1343

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DB 1344 TTTTGGCCACCGCTAACCTGCTCTTTTAACTGCTTTTAAACCAATATTTATAAACCCTTG 1403

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; Sequence 1, Application US/09223535
; Patent No. 6232525
; GENERAL INFORMATION:
; APPLICANT: Ryals, John
; APPLICANT: Uknes, Scott
; APPLICANT: Ward, Eric
; APPLICANT: Delaney, Terry
; APPLICANT: Lawton, Kay
; APPLICANT: Weymann, Kris
; APPLICANT: Steiner, Henry-York
; APPLICANT: Maleck, Klaus

; TITLE OF INVENTION: Method For Breeding Disease Resistance
; TITLE OF INVENTION: Into Plants
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6232525artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/223,535
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/992,801
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/165,248
; FILING DATE: 10-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/002,285
; FILING DATE: 08-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: CGC1673/CIP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14113 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "PR-1/luc construct"
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Job time : 342 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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(without alignments)

11960.100 Million cell updates/sec

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Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 6382046

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	4549	94.7	10003	10	US-09-845-064-21 Sequence 21, Appl
4	4531.4	94.3	5614	10	US-09-845-064-16 Sequence 16, Appl
5	4531.4	94.3	5971	10	US-09-845-064-3 Sequence 3, Appl
6	4531.4	94.3	6016	10	US-09-845-064-4 Sequence 4, Appl
7	4531.4	94.3	6016	10	US-09-845-064-6 Sequence 6, Appl
8	4531.4	94.3	6017	10	US-09-845-064-5 Sequence 5, Appl
9	4531.4	94.3	6017	10	US-09-845-064-7 Sequence 7, Appl
10	4531.4	94.3	6767	10	US-09-845-064-8 Sequence 8, Appl
11	4531.4	94.3	6767	10	US-09-845-064-9 Sequence 9, Appl
12	4531.4	94.3	6865	10	US-09-845-064-13 Sequence 13, Appl
13	4531.4	94.3	7503	10	US-09-845-064-17 Sequence 17, Appl
14	4531.4	94.3	7503	10	US-09-845-064-19 Sequence 19, Appl

15	4531.4	94.3	8289	10	US-09-845-064-55	Sequence 55, Appl
16	4531.4	94.3	8654	10	US-09-845-064-14	Sequence 14, Appl
17	4531.4	94.3	8987	10	US-09-845-064-22	Sequence 22, Appl
18	4531.4	94.3	9143	10	US-09-845-064-12	Sequence 12, Appl
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22	4528.2	94.2	9390	10	US-09-845-064-18	Sequence 18, Appl
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45	2536.2	52.8	17752	13	US-10-250-821-28	Sequence 28, Appl

ALIGNMENTS

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; Publication No. US20030175976A1  
; GENERAL INFORMATION:  
; APPLICANT: MERISTEM THERAPEUTICS  
; TITLE OF INVENTION: CLEAN SYNTHETIC VECTORS, PLASMIDS, TRANSGENIC PLANTS  
; TITLE OF INVENTION: AND PLANT PARTS CONTAINING SAID VECTORS, AND THEIR  
; TITLE OF INVENTION: METHODS OF PRODUCTION  
; FILE REFERENCE: SynVec1  
; CURRENT APPLICATION NUMBER: US/09/845,064  
; CURRENT FILING DATE: 2001-04-27  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 10  
; LENGTH: 4805  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
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; OTHER INFORMATION: NPT III gene coding for neomycin  
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Qy 2641 CCAGGCCCCACGGCAAGTATTTGGGCAAGGGTCTGCTGTTATTCGTCAGGCAAGATTC 2700  
Db 2641 CCAGGCCCCACGGCAAGTATTTGGGCAAGGGTCTGCTGTTATTCGTCAGGCAAGATTC 2700  
Qy 2701 GGAATACCAAGTACGAGAAGGA CGGCGCAGACGCTCTACGGGACCGACTTTCATTTCCCGATA 2760  
Db 2701 GGAATACCAAGTACGAGAAGGA CGGCGCAGACGCTCTACGGGACCGACTTTCATTTCCCGATA 2760  
Qy 2761 AGTGGATTATCTGGACACCAAGGCCAGGCGGCTCAATCAGGAATAGGGCACAATTG 2820  
Db 2761 AGTGGATTATCTGGACACCAAGGCCAGGCGGCTCAATCAGGAATAGGGCACAATTG 2820  
Qy 2821 CCCCGGCGTGAAGTCGGGGCAATCCCGCAAGAGGGTGAATGAATCGGACGCTTTGACCGGA 2880  
Db 2821 CCCCGGCGTGAAGTCGGGGCAATCCCGCAAGAGGGTGAATGAATCGGACGCTTTGACCGGA 2880  
Qy 2881 AGGCATACGGCAAGAACTGATCGACGCGGGGTTTTCCGCGGAGGATGCCGAACCATCG 2940  
Db |||||

Db 2881 AGGCATACGGCAAGAACTGATCGACGCGGGGTTTTCCGCCGAGGATGCCGAACCATCG 2940  
Qy 2941 CAAAGCCGACCGCTCATGCGTGGCCCGCGAAAACTTCCAGTCCGTCGGCTCGATGTGCC 3000  
Db 2941 CAAAGCCGACCGCTCATGCGTGGCCCGCGAAAACTTCCAGTCCGTCGGCTCGATGTGCC 3000  
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Db 3061 CGGCATCGCCCGCTGGAGCGTTCGCTCGTCTCGAACAGGAGGGCGAGGTTTGGCGA 3120  
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Db 3121 AGTCGATGACCATCGACAGCGAGGAACTATGACGACCAAGAGCGAAAAACCGCCGGCG 3180  
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Db 3181 AGGACCTGGCAAAACAGGTCAGCGAGGCCAAAGCAGCGCGGTTTGTGAAACACACGAAGC 3240  
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Qy 3481 ACAGGAAGCGCACCCCTATCGGCGAGCCGATCACTTTCAGCTTCTACGAGCTTTCGCGAG 3540  
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Db 3961 TGAACAACGCTGGGTCAATGATGACCTGTGCTGCAAAACCTAGGGCTTGTGGGT 4020





Db 61 AAAGCGCTGAAGCCGTGTGCGAGACACCGCGCGCGCGCGTGTGTGGATACCTCGCGG 120  
Qy 121 AAAATTGGCCCTCACTGACAGATGAGGGCGGACGTTGACACTTGAGGGCGCGACTCAC 180  
Db 121 AAAATTGGCCCTCACTGACAGATGAGGGCGGACGTTGACACTTGAGGGCGCGACTCAC 180  
Qy 181 CCGCGCGGGGTTGACAGATGAGGGCGAGGCTCGATTTGGCGCGGCGACGTGAGCTGGC 240  
Db 181 CCGCGCGGGGTTGACAGATGAGGGCGAGGCTCGATTTGGCGCGGCGACGTGAGCTGGC 240  
Qy 241 CAGCTCGCAAAATCGCGAAAACGCTGATTTTACGCGAGTTTCCCAACAGATGATGGGA 300  
Db 241 CAGCTCGCAAAATCGCGAAAACGCTGATTTTACGCGAGTTTCCCAACAGATGATGGGA 300  
Qy 301 CAAAGCTTGGGGAATGAGTGGCCCTCGGATATTGACACTTGAGGGCGGCGACTTACTGACAGAT 360  
Db 301 CAAAGCTTGGGGAATGAGTGGCCCTCGGATATTGACACTTGAGGGCGGCGACTTACTGACAGAT 360  
Qy 361 GAGGGGCGGATCCTTGTGACHACTTGAGGGCGAGGTGTGACAGATGAGGGGCGCACTTAT 420  
Db 361 GAGGGGCGGATCCTTGTGACHACTTGAGGGCGAGGTGTGACAGATGAGGGGCGCACTTAT 420  
Qy 421 TGCATTTTGAAGGGCTGTCCACAGGCGAGAAATCCAGCATTTTGAAGGGTTTCCGCGCGT 480  
Db 421 TGCATTTTGAAGGGCTGTCCACAGGCGAGAAATCCAGCATTTTGAAGGGTTTCCGCGCGT 480  
Qy 481 TTTTTCGGCACCCCTAAACCTGTCTTTTAACTCTCTTTTAAACCAATATTTATAAACTTG 540  
Db 481 TTTTTCGGCACCCCTAAACCTGTCTTTTAACTCTCTTTTAAACCAATATTTATAAACTTG 540  
Qy 541 TTTTAAACAGGGCTCGCCCTGTGCGCGTGACCGCGACCGCGAAGGGGGTGCCTCC 600  
Db 541 TTTTAAACAGGGCTCGCCCTGTGCGCGTGACCGCGACCGCGAAGGGGGTGCCTCC 600  
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Db 601 CTTCTCGAACCTCCCGAAAGATATGCGGTGTGAATACCGCACAGATGCGTAAGGAGA 660  
Qy 661 AAATACCGATCAGGGCTCTTCGGCTCTCCCTCACTGACTCGCTGCGCTCGGTCGTT 720  
Db 661 AAATACCGATCAGGGCTCTTCGGCTCTCCCTCACTGACTCGCTGCGCTCGGTCGTT 720  
Qy 721 CGGCTCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAAATACGGTTATCCACAGAATCA 780  
Db 721 CGGCTCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAAATACGGTTATCCACAGAATCA 780  
Qy 781 GGGGATAACGAGGAAAGAACATGTGAGCAAAAGGCGCAGAAAGCCAGGAACCGTAAA 840  
Db 781 GGGGATAACGAGGAAAGAACATGTGAGCAAAAGGCGCAGAAAGCCAGGAACCGTAAA 840  
Qy 841 AAGGCCGCTGTGCTGGCGTTTTTCCATAGGCTCCGCCCTCCCTGACGAGATCACAAAAAT 900  
Db 841 AAGGCCGCTGTGCTGGCGTTTTTCCATAGGCTCCGCCCTCCCTGACGAGATCACAAAAAT 900  
Qy 901 CGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAGATACCAAGGCTTTCC 960  
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Qy 961 CTTGGAAGCTCCCTCGTGGCTCTCCTGTTCCGACCCCTGCGGTTACCGGATACCTGTCC 1020  
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Db 1021 GCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGATGATCTCAGT 1080  
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Db 1141 CGCTGCGCTTATCCGGTAACTATCGTCTTGAAGTCCAAACCCGGTAAAGACGACTTATCG 1200

Qy 1201 CCATCGCAGCAGCCTTCTACCATAAATCCGCGATAAACCCAGCGAAACCAATTTGAGGTGAT 1260  
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Qy 1261 AGGTAAGATTATACCGAGGTATGAAAAACGAGAAATTCGACCTTTACAGAAATTAATCTATGA 1320  
Db 1261 AGGTAAGATTATACCGAGGTATGAAAAACGAGAAATTCGACCTTTACAGAAATTAATCTATGA 1320  
Qy 1321 AGCGCCATATTTAAAAAGCTTACCAAGCAAGAGGATGAAGAGATGAGGAGGAGAGATTG 1380  
Db 1321 AGCGCCATATTTAAAAAGCTTACCAAGCAAGAGGATGAAGAGATGAGGAGGAGAGATTG 1380  
Qy 1381 CTTTGAATATATTGACAATCTGATAAGATAATACTCTTTTATATAGAGATATCGCCG 1440  
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Qy 1501 GGGCAAGCATAAAACTTGCATGGAATAATGCTTGAACCCAGGACAATACTTATAG 1560  
Db 1501 GGGCAAGCATAAAACTTGCATGGAATAATGCTTGAACCCAGGACAATACTTATAG 1560  
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Db 1561 CTTGTAATTTTACCAAAATTTGTTTCAAAATCGGCTCGCTGATATCTATGATACG 1620  
Qy 1621 CCAACTTTGAAAAACAACTTTGAAAAAGCTGTTTTCTGTTATTTAAGGTTTTAGAAATGCAA 1680  
Db 1621 CCAACTTTGAAAAACAACTTTGAAAAAGCTGTTTTCTGTTATTTAAGGTTTTAGAAATGCAA 1680  
Qy 1681 GGAACAGTCAATGGAAGTTGCTGTTGTTATTAATAGCTTCTTGGGCTACTTTAAATACT 1740  
Db 1681 GGAACAGTCAATGGAAGTTGCTGTTGTTATTAATAGCTTCTTGGGCTACTTTAAATACT 1740  
Qy 1741 GTAGAAAAAGAGAAAGAAATAATAATGCTTAAATGAGAATAATCACCGGAAATGAAAAA 1800  
Db 1741 GTAGAAAAAGAGAAAGAAATAATAATGCTTAAATGAGAATAATCACCGGAAATGAAAAA 1800  
Qy 1801 ACTGATCGAAAAATAATACCGCTGCGTAAAAAGATACGGAAGGAATGCTCTGCTAAGGTATA 1860  
Db 1801 ACTGATCGAAAAATAATACCGCTGCGTAAAAAGATACGGAAGGAATGCTCTGCTAAGGTATA 1860  
Qy 1861 TAAGCTGTTGGGAGAAATGAAAACTTATTTAAAAATGACGACAGCGGTTATAAGG 1920  
Db 1861 TAAGCTGTTGGGAGAAATGAAAACTTATTTAAAAATGACGACAGCGGTTATAAGG 1920  
Qy 1921 GACCACCTATGATGTGAAACGGGAAAGGACATGATGCTATGCTGGAAGGAAAGCTGCC 1980  
Db 1921 GACCACCTATGATGTGAAACGGGAAAGGACATGATGCTATGCTGGAAGGAAAGCTGCC 1980  
Qy 1981 TGTTCAAAAGGTCCTGCACTTTGAAACGGCATGATGCTCGAGCAATCTGCTCATAGTGA 2040  
Db 1981 TGTTCAAAAGGTCCTGCACTTTGAAACGGCATGATGCTCGAGCAATCTGCTCATAGTGA 2040  
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Db 2041 GGGCGATGCGCTCTTGTCTCGGAAAGATGAAAGATGAACAAAGCCCTGAAAAAGATTAT 2100  
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Qy 2161 TACGAATAGCTTAGACAGCGCTTAGCGGAATTTGGAATTAATTAAGATCCCGGCGAGCTGTA 2220  
Db 2161 TACGAATAGCTTAGACAGCGCTTAGCGGAATTTGGAATTAATTAAGATCCCGGCGAGCTGTA 2220  
Qy 2221 CGATGTGGAATTCGGAATACTCGGAAAGACACTCCATTTAAAGATCCCGCGAGCTGTA 2280  
Db 2221 CGATGTGGAATTCGGAATACTCGGAAAGACACTCCATTTAAAGATCCCGCGAGCTGTA 2280

QY	2281	TGATTTTTTAAAGACGAAAGCCCGAAGAGGAACCTGTCTTTTTCCACGCGACCTGGG	2340
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QY	2341	AGACAGCAACATCTTTGTGAAAGATGSCAAAGTAAGTGGCTTTATTGATCTTGGGAGAAG	2400
Db	2341		
QY	2401	CGGAGGCGGACAAAGTGGTATGACATTCGCTCTCTGGGTCGGTTCGATCAGGAGGATAT	2460
Db	2401		
QY	2461	CGGGGAAGAACAGTATCTCGAGCTATTTTTTGACTTACTGGGATCAAGCTCGATTGGGA	2520
Db	2461		
QY	2521	GAAAAATAAAATATTATATTTTACTGGATGAATTTGTTTACTAGATCTAGATGTCGCAACG	2580
Db	2521		
QY	2581	ATCGCGGCGAAGAGGAGCGGACCGACTTCTTCGCGATCAAGTGTTCGCTCTCAGG	2640
Db	2581		
QY	2641	CCGAGGCCACGCGCAAGTATTTGGGCAAGGGTCGCTGGTATTCTGTCAGGCAAGATTC	2700
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QY	2701	GGAAATACCAAGTACGAGAAGACGGCCAGACGGTCTACGGGACCGACTTCATTGCCGATA	2760
Db	2701		
QY	2761	AGGTGGATTATCTGGACACCAAGGCACAGCGGGTCAAAATCAGGAATAAGGGCACATTG	2820
Db	2761		
QY	2821	CCCCGGGTCAGTCCGGGCAATCCCGCAAGAGGGTGAATGAATCGGACGCTTTGACCGGA	2880
Db	2821		
QY	2881	AGGCATACAGGCAAGAACTGATCGACCGGGTTTTCCGCGGAGGATGCGAAACCATCG	2940
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QY	2941	CAAGCCGACCGTCAATCGTGCGCCCGCGAAACCTTCCAGTCCGCTCGATGCTCC	3000
Db	2941		
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QY	3061	CGCCATCGGCGCGCTGGAGCGTTTCGCTCGAACAGGAGCGCGCAGGTTTGGCGA	3120
Db	3061		
QY	3121	AGTCGATGACATCGACACCGGAGAACTATGACGACCAAGAACGAAAAACCGCCGGCG	3180
Db	3121		
QY	3181	AGGACCTGGCAAAACAGGTACGCGAGCGCACAGCGTGCCTGCTGAAAACACACGAAGC	3240
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QY	3241	AGCAGATCAAGGAAATGCAGCTTTCTTGTTCGATATTGCGCCGTGGCGGACACGATGC	3300
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QY	3301	GAGCGATGCCAAACGACAGCGCCGCTCTGCGCTTGTCAACCACCGGCACCAAGAAAAATCC	3360
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QY	3361	CGCGGAGGCGCTGCAAAACAAAGTCTATTTTCCACGTCACCAAGGACGTGAAGATCACCT	3420
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Db	3361	CGCGGAGGCGCTGCAAAACAAAGTCTATTTTCCACGTCACCAAGGACGTGAAGATCACCT	3420
QY	3421	ACACCGGCGTTCAGACTGCGGGCCGACGATGACGAAGTGTGTGGCAGAGGTGTTGGAGT	3480
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Db	3481		
QY	3541	ACCTGGGCTGGTCGATCAATGGCCGCTATTACAGAAAGCCGAGGAATGCTCTCGCGCC	3600
Db	3541		
QY	3601	TACAGCGAGCGGATGGGCTTACGTCGACCGCGTTGGGACCTTGGATCGGTGTCG	3660
Db	3601		
QY	3661	TGCTGCACCGCTTCCGCGTCTGGACCGTGGCAAGAAAAAGTCCCGTTGCCAGGTCCTGA	3720
Db	3661		
QY	3721	TCGACGAGGAAATCGTCTGCTGTTTGTCTGGCGACCACTACAGAAATTCATATGGGAGA	3780
Db	3721		
QY	3781	AGTACCGGAAGCTGTCGCGACGGCCGAGCGGATGTTCCACTATTTTTCAGCTCCGACCGGG	3840
Db	3781		
QY	3841	AGCCGTACCCGCTCAAGCTTGGAAACCTTCGCGCTCATGTGCGGATCGEATTTCCACCGCG	3900
Db	3841		
QY	3901	TGAAGAAGTGGCGAGCAGGTTCGGCAAGCCTTCGCGCTCATGTGCGGATCGGATTTCCACCGCG	3960
Db	3901		
QY	3961	TGAAACAACGCTGGGTCAATGATGACTGCTGGTGAATTCGAAACCGCTTAGGGCTTTGCGGGT	4020
Db	3961		
QY	4021	CAGTTCGCGTGGGGTTCAGCAGCCAGCGCTTTTACTGGCATTTCTTAGGTTGACGCTCTT	4080
Db	4021		
QY	4081	CTGATCGGCTGCTGTATCGAGTGGTGAATTTGTGCGAGCTCCCGTTCGGGAGCTGTT	4140
Db	4081		
QY	4141	GGCTGGCTGGCGAGGATATATTGGTGTAAACAAATTTGACGCTTAGACAACTTAATA	4200
Db	4141		
QY	4201	ACACATTTGGGAGCTTTTAACTACTGCGGCTATCCCGCGGGGATATCCATAGGCCCCG	4260
Db	4201		
QY	4261	ATCTAGTAAACATAATGACACCGCGCGATAATTTATCTCTAGTTTTCGCGCTATTTTTG	4320
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QY	4321	TTTTCTATCGCGTATTAAATGATTAATTCGGGACCTCTAATCAATAAAACCCATCTCATA	4380
Db	4321		
QY	4381	AATAACGTCATGATACATGTTAAATTTATTTATTTATTTATTTATTTATTTATTTATTTAT	4440
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QY	4441	ATGATATATCATCGCAAGACCGGCAACAGGATTCATCTTTAAGAAACCTTTATTTGCAAAATG	4500
Db	4441		

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RESULT 3

US-09-845-064-21  
; Sequence 21, Application US/09845064  
; Publication No. US20030175976A1  
; GENERAL INFORMATION:  
; APPLICANT: MERISTEM THERAPEUTICS  
; TITLE OF INVENTION: CLEAN SYNTHETIC VECTORS, PLASMIDS, TRANSGENIC PLANTS  
; TITLE OF INVENTION: AND PLANT PARTS CONTAINING SAID VECTORS, AND THEIR  
; TITLE OF INVENTION: METHODS OF PRODUCTION  
; FILE REFERENCE: SynVec1  
; CURRENT APPLICATION NUMBER: US/09/845,064  
; CURRENT FILING DATE: 2001-04-27  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 21  
; LENGTH: 10003  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:Plasmid  
; OTHER INFORMATION: pmrT1210  
; NAME/KEY: rep origin  
; LOCATION: (1)..(654)  
; OTHER INFORMATION: Origin of replication ori RK2  
; FEATURE:  
; NAME/KEY: rep origin  
; LOCATION: (655)..(1263)  
; OTHER INFORMATION: Origin of replication ori ColeI  
; FEATURE:  
; NAME/KEY: gene  
; LOCATION: (1264)..(2603)  
; OTHER INFORMATION: NPT III gene coding for neomycin  
; OTHER INFORMATION: phosphotransferase and kanamycin resistance  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (2604)..(4098)  
; OTHER INFORMATION: TrfA locus from RK2 coding for two proteins, p285  
; OTHER INFORMATION: and p382, enabling the increase of the replication  
; OTHER INFORMATION: rate  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (4106)..(4271)  
; OTHER INFORMATION: T-DNA left border  
; FEATURE:  
; NAME/KEY: terminator  
; LOCATION: (4272)..(4559)  
; OTHER INFORMATION: No. US20030175976A1alaine synthetase terminator  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (4559)..(4572)  
; OTHER INFORMATION: MCS multiple cloning site  
; FEATURE:  
; NAME/KEY: gene  
; LOCATION: (4594)..(5169)  
; OTHER INFORMATION: Bar gene coding for phosphinothricine  
; OTHER INFORMATION: acetyltransferase and glufosinate resistance  
; FEATURE:  
; NAME/KEY: intron  
; LOCATION: (5170)..(5704)  
; OTHER INFORMATION: Rice Actin Intron  
; FEATURE:

; NAME/KEY: promoter  
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; OTHER INFORMATION: Rice Actin Promoter  
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; NAME/KEY: misc feature  
; LOCATION: (6646)..(6672)  
; OTHER INFORMATION: MCS multiple cloning site  
; FEATURE:  
; NAME/KEY: promoter  
; LOCATION: (6672)..(7107)  
; OTHER INFORMATION: High Molecular Weight Glutenin promoter from wheat  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (7107)..(7169)  
; OTHER INFORMATION: MCS multiple cloning site  
; FEATURE:  
; NAME/KEY: intron  
; LOCATION: (7169)..(7687)  
; OTHER INFORMATION: Rice Actin Intron  
; FEATURE:  
; NAME/KEY: gene  
; LOCATION: (7688)..(9496)  
; OTHER INFORMATION: GUS gene coding for beta glucuronidase  
; FEATURE:  
; NAME/KEY: terminator  
; LOCATION: (9497)..(9823)  
; OTHER INFORMATION: No. US20030175976A1alaine synthetase terminator  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (9823)..(9996)  
; OTHER INFORMATION: T-DNA right border  
; US-09-845-064-21  
  
Query Match 94.7%; Score 4549; DB 10; Length 10003;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 4549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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Db 1 CCGGGCTGTTGCCCTCGCCCTGCGGCTGGGCTGGGCGCGCTTATGGCCCTGCAAAACGCGCCAG 60  
  
QY 61 AAACGCTGCGAAGCGCTGTGCGAGACACCGCGGCGCGCGCTTGTGANTACTCTGCGG 120  
Db 61 AAACGCTGCGAAGCGCTGTGCGAGACACCGCGGCGCGCGCTTGTGANTACTCTGCGG 120  
  
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Db 121 AAAAATTGGCCCTCACTGACAGATGAGGGCGGCGAGCTTGACACTTGAGGGCGCGACTCAC 180  
  
QY 181 CCGGCGCGCGCTTGACAGATGAGGGCGAGGCTCGATTTCGGCGCGCGAGCTGGAGCTGGC 240  
Db 181 CCGGCGCGCGCTTGACAGATGAGGGCGAGGCTCGATTTCGGCGCGCGAGCTGGAGCTGGC 240  
  
QY 241 CAGCCTCGCAAAATCGCGGAAACCGCTGATTTTACCGAGTTTCCACAGATGATGGA 300  
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QY 301 CAAGCTGGGGGATAAGTGCCTCGCGTATTGACACTTGAGGGCGCGAGCTTACTGACAGAT 360  
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QY 361 GAGGGCGCGATCCTTTGACACTTGAGGGCGAGAGTCTGACAGATGAGGGCGCGACCTAT 420  
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Qy	541	TTTTTAACAGGGCTGCGCCTGTGCGGTGACCGCAGCCGAAAGGGGGTGC	600
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Qy	601	CTTCTCGAACCCCTCCCGGAAGGTATGCGGTGTGAATACCGCACAGATCGTAAGGAGA	660
Db	601	CTTCTCGAACCCCTCCCGGAAGGTATGCGGTGTGAATACCGCACAGATCGTAAGGAGA	660
Qy	661	AAATACCGCATAGGGCGCTCTCGGCTTCTCGCTCACTGACTCGCTCGCTCGTTCGTT	720
Db	661	AAATACCGCATAGGGCGCTCTCGGCTTCTCGCTCACTGACTCGCTCGCTCGTTCGTT	720
Qy	721	CGGCTGGGCGAGCGGTATCAGCTCACTCAAGGCGGTAAATACGTTTATCCACAGAAATCA	780
Db	721	CGGCTGGGCGAGCGGTATCAGCTCACTCAAGGCGGTAAATACGTTTATCCACAGAAATCA	780
Qy	781	GGGGATAACCGAGAAAGAACATGTGAGCAAAAGGCCAGCAAGGCCAGGAACCGTA	840
Db	781	GGGGATAACCGAGAAAGAACATGTGAGCAAAAGGCCAGCAAGGCCAGGAACCGTA	840
Qy	841	AAGGCGCGTGTGCGGTTTTTCCATAGGCTCGGCCCTCGCTGACGAGCATCA	900
Db	841	AAGGCGCGTGTGCGGTTTTTCCATAGGCTCGGCCCTCGCTGACGAGCATCA	900
Qy	901	CGAGCTCAAGTCAGAGGTGCGGAACCCGACAGGACTATAAGATACCAAGGCTTTCCC	960
Db	901	CGAGCTCAAGTCAGAGGTGCGGAACCCGACAGGACTATAAGATACCAAGGCTTTCCC	960
Qy	961	CCTGGAAGCTCCCTCGTGCCTCTCTCTGTTCCGACCCCTGCGCTTACCGGATACCTGTCC	1020
Db	961	CCTGGAAGCTCCCTCGTGCCTCTCTCTGTTCCGACCCCTGCGCTTACCGGATACCTGTCC	1020
Qy	1021	GCCTTTCTCCCTTCGGGAAGGTGGCGCTTCTCATAGCTCA	1080
Db	1021	GCCTTTCTCCCTTCGGGAAGGTGGCGCTTCTCATAGCTCA	1080
Qy	1081	TCGGTGTAGTCTCGCTCCAGCTGGCTGTGTCAGCAACCCCGCTTCAGCCCGAC	1140
Db	1081	TCGGTGTAGTCTCGCTCCAGCTGGCTGTGTCAGCAACCCCGCTTCAGCCCGAC	1140
Qy	1141	CGCTGCGCCTTATCCGGTAACATCGTCTTGAGTCCAAACCGGTGAACACGACTTATCG	1200
Db	1141	CGCTGCGCCTTATCCGGTAACATCGTCTTGAGTCCAAACCGGTGAACACGACTTATCG	1200
Qy	1201	CCTGCGCAGAGCTTCTACATAATCCGGATAAACCCGACCCATTTGAGGTGAT	1260
Db	1201	CCTGCGCAGAGCTTCTACATAATCCGGATAAACCCGACCCATTTGAGGTGAT	1260
Qy	1261	AGGTAAAGATTATACCGAGGTATGAAACGAGAAATGGACCTTTACAGAAATTTACTCTATGA	1320
Db	1261	AGGTAAAGATTATACCGAGGTATGAAACGAGAAATGGACCTTTACAGAAATTTACTCTATGA	1320
Qy	1321	AGCGCCATATTTAAAAAGCTACCAAGACGAAGAGGATGAAGAGGATGAGGAGGAGATTG	1380
Db	1321	AGCGCCATATTTAAAAAGCTACCAAGACGAAGAGGATGAAGAGGATGAGGAGGAGATTG	1380
Qy	1381	CCTTGAATATATTGACAAATCTGATAAGATAATACATCTTTTATATAGAATATCCCG	1440
Db	1381	CCTTGAATATATTGACAAATCTGATAAGATAATACATCTTTTATATAGAATATCCCG	1440
Qy	1441	TATGTAGGATTTTCCAGGGGCAAGGCATAGGACGCGCTTATCAATATATCTATAGAAT	1500
Db	1441	TATGTAGGATTTTCCAGGGGCAAGGCATAGGACGCGCTTATCAATATATCTATAGAAT	1500
Qy	1501	GGGCAAGACATAAAAACTTGCATGGAATAATGCTTTGAAACCCAGGACAAATAACCTTATAG	1560
Db	1501	GGGCAAGACATAAAAACTTGCATGGAATAATGCTTTGAAACCCAGGACAAATAACCTTATAG	1560
Qy	1561	CTTGTAATTTCTACAAAAATTTGGTTTCAAAAATCGGCTCGCTCGATATGTTATACG	1620
Db	1561	CTTGTAATTTCTACAAAAATTTGGTTTCAAAAATCGGCTCGCTCGATATGTTATACG	1620
Qy	1621	CCAACTTTGAAAAACAACCTTTGAAAAAGCTGTTTCTGTTATTTAAGGTTTTTAGAATGCAA	1680

Db	1621	CCAACTTTGAAAAACAACCTTTGAAAAAGCTGTTTCTGTTATTTAAGGTTTTTAGAATGCAA	1680
Qy	1681	GGAACTGTAATTTGGAGTTCTGTTTATTAATAGCTTCTTGGGTATCTTTAAATACT	1740
Db	1681	GGAACTGTAATTTGGAGTTCTGTTTATTAATAGCTTCTTGGGTATCTTTAAATACT	1740
Qy	1741	GTAGAAAAAGAGGAAGAAATAAATAGCTAAAAATGAGAAATATCACCGAAATGAAAAA	1800
Db	1741	GTAGAAAAAGAGGAAGAAATAAATAGCTAAAAATGAGAAATATCACCGAAATGAAAAA	1800
Qy	1801	ACTGATCGAAAAATACCGTGCCTAAAAATACGGAAGGAATGTCTCTGCTAAGGTATA	1860
Db	1801	ACTGATCGAAAAATACCGTGCCTAAAAATACGGAAGGAATGTCTCTGCTAAGGTATA	1860
Qy	1861	TAAGCTGGTGGGAGAAATGAAAACTTATTTAAAAATGACGACAGCGGTATTAAGG	1920
Db	1861	TAAGCTGGTGGGAGAAATGAAAACTTATTTAAAAATGACGACAGCGGTATTAAGG	1920
Qy	1921	GACCACTATGATGTGAAACGGGAAAGGACATGATGCTATGGCTGGAAGGAAGCTGCC	1980
Db	1921	GACCACTATGATGTGAAACGGGAAAGGACATGATGCTATGGCTGGAAGGAAGCTGCC	1980
Qy	1981	TGTTCCAAAAGTCTCTGACCTTTGAACGGCATGATGGCTGGAGCAATCTGCTCATAGTGA	2040
Db	1981	TGTTCCAAAAGTCTCTGACCTTTGAACGGCATGATGGCTGGAGCAATCTGCTCATAGTGA	2040
Qy	2041	GGCGATGGGCTCTTTCGGAAGAGATGAAAGATGAAAGCCCTGAAAAGATTAT	2100
Db	2041	GGCGATGGGCTCTTTCGGAAGAGATGAAAGATGAAAGCCCTGAAAAGATTAT	2100
Qy	2101	CGAGCTGTATGCGGAGTGATCAGGCTCTTTCACCTCCATCGACATATCGGATTTGCCCTA	2160
Db	2101	CGAGCTGTATGCGGAGTGATCAGGCTCTTTCACCTCCATCGACATATCGGATTTGCCCTA	2160
Qy	2161	TACGAATAGCTTACAGACGCGCTTACCGAATTTGGATTTACTTACTGAATAACGATCTGGC	2220
Db	2161	TACGAATAGCTTACAGACGCGCTTACCGAATTTGGATTTACTTACTGAATAACGATCTGGC	2220
Qy	2221	CGATGTGGATTTGCGAAAACTGGGGAAGAGACATCCATTTAAAGATCCGCGGAGCTGTA	2280
Db	2221	CGATGTGGATTTGCGAAAACTGGGGAAGAGACATCCATTTAAAGATCCGCGGAGCTGTA	2280
Qy	2281	TGATTTTTTAAAGACGGAAAGCCCGAAGAGAACTTGTCTTTCCACCGCGACCTGGG	2340
Db	2281	TGATTTTTTAAAGACGGAAAGCCCGAAGAGAACTTGTCTTTCCACCGCGACCTGGG	2340
Qy	2341	AGACAGCAACATCTTTGTGAAAGATGGCAAAAGTAAGTGGCTTTTATTTGATCTTGGGAGAAG	2400
Db	2341	AGACAGCAACATCTTTGTGAAAGATGGCAAAAGTAAGTGGCTTTTATTTGATCTTGGGAGAAG	2400
Qy	2401	CGGCGGCGGACAAGTGTATGACATTTGCTTCTGCTCCGCTCGATCAGGGAGGATAT	2460
Db	2401	CGGCGGCGGACAAGTGTATGACATTTGCTTCTGCTCCGCTCGATCAGGGAGGATAT	2460
Qy	2461	CGGGAAGAACAGTATGTCTGAGCTATTTTGTGACTTACTCGGGATCAAGCTCTGATTCGGA	2520
Db	2461	CGGGAAGAACAGTATGTCTGAGCTATTTTGTGACTTACTCGGGATCAAGCTCTGATTCGGA	2520
Qy	2521	GAATAAAAAATATATATTTTACTGGAATGAATTTTGTAGTACTAGATGTGGCGCAACG	2580
Db	2521	GAATAAAAAATATATATTTTACTGGAATGAATTTTGTAGTACTAGATGTGGCGCAACG	2580
Qy	2581	ATGCGCGGACAAGAGGAGCGCACCGACTTCTTCCGATCAAGTGTGCTGCTCAGG	2640
Db	2581	ATGCGCGGACAAGAGGAGCGCACCGACTTCTTCCGATCAAGTGTGCTGCTCAGG	2640
Qy	2641	CCGAGGCCCAAGCAAGTATTTGGGCAAGGGGTGCTGTTTCTGTCAGGCGCAAGATTC	2700
Db	2641	CCGAGGCCCAAGCAAGTATTTGGGCAAGGGGTGCTGTTTCTGTCAGGCGCAAGATTC	2700
Qy	2701	GGAAATACAAAGTACGAGAAAGGACGGGCGACGCTCTACCGGACCGACTTCAATCCCGGATA	2760

Db 2701 GGAATACCAAGTACGAGAGGA CGGCCAGACGGTCTACGGGACCGACTTCATTCTGCCGATA 2760  
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Db 2761 AGGTGGATTATCTGGACACCAAGGCA CAGGCGGGTCAAAATCAGGAATAAGGGCACATTG 2820  
Qy 2821 CCCGGCGTGTAGTCCGGGCGAATCCCGCAAGAGAGGTGAATGAATCGGACGTTTGA CCGGA 2880  
Db 2821 CCCGGCGTGTAGTCCGGGCGAATCCCGCAAGAGAGGTGAATGAATCGGACGTTTGA CCGGA 2880  
Qy 2881 AGGCATACAGCAAGAACTGATCGACCGGGTTTTCCGCGGAGGATGCCGAACCATCG 2940  
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Qy 3001 AGCAAGCTACGGCCAAAGATCGAGCGGACACGCTGCTCTCGAACAGGAGCGGAGGTTTGGCGA 3060  
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Qy 3421 ACACCGCGTGTAGCTCGGGCGACGATGACGAACTGGTGTGGCAGCAGGTGTGGAGT 3480  
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Qy 3481 ACGGAGCGCACCCCTATCGGCGAGCGGATCACTTTCAGTTCTACGAGCTTGGCCAGG 3540  
Db 3481 ACGGAGCGCACCCCTATCGGCGAGCGGATCACTTTCAGTTCTACGAGCTTGGCCAGG 3540  
Qy 3541 ACCTGGCTGTGTGATCAATGGCGGTATTAACGAAAGGCGAGGAATGCTGTGCGGCC 3600  
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Qy 3721 TCAGCAGGAAATCGTGTGTGTTTGTCTGGCAGCACTACAGAAATTCATATGGGAGA 3780  
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Qy 3781 AGTACCGCAAGCTGTGCCCGACGGCCCGACGGAATGTTGACTATTTTCAGTCTCGACCGGG 3840  
Db 3781 AGTACCGCAAGCTGTGCCCGACGGCCCGACGGAATGTTGACTATTTTCAGTCTCGACCGGG 3840

Qy 3841 AGCGGTACCCGCTCAAGCTGGAAACCTTCCGCTCATGTCCGGATCGGATTCACCCGCG 3900  
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Qy 4081 CTGATGGGCTGCTGTATCGAGTGGTGAATTTGTCGGAGCTGCGGTCCGGGAGCTGTT 4140  
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Db 4141 GGCTGCTGTGGCAGGATATTTGGTGTAAACAAATTTGACGCTTAGACAACTTAATA 4200  
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Db 4201 ACACATTTGGCGACGTTTTTAATGTAATGCTGGGGCTATCCCCGGGGGATATCCATAGGCCG 4260  
Qy 4261 ATCTAGTAACATTAATGACACCGCGCGGATAAATTTACTAGTGTGGCGCTATATTTG 4320  
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Db 4321 TTTTCTATCGCGTATTAATGTAATTTGGGACCTCTATATAAAACCCATCTCATA 4380  
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RESULT 4  
US-09-845-064-16  
; Sequence 16, Application US/09845064  
; Publication No. US20030175976A1  
; GENERAL INFORMATION:  
; APPLICANT: MERISTEM THERAPEUTICS  
; TITLE OF INVENTION: CLEAN SYNTHETIC VECTORS, PLASMIDS, TRANSGENIC PLANTS  
; TITLE OF INVENTION: AND PLANT PARTS CONTAINING SAID VECTORS, AND THEIR  
; TITLE OF INVENTION: METHODS OF PRODUCTION  
; FILE REFERENCE: SynVec1  
; CURRENT APPLICATION NUMBER: US/09/845,064  
; CURRENT FILING DATE: 2001-04-27  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 16  
; LENGTH: 5614  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Plasmid  
; OTHER INFORMATION: pmr1202  
; FEATURE:  
; NAME/KEY: rep\_origin

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; LOCATION: (1)...(654)
; OTHER INFORMATION: Origin of replication ori RK2
; FEATURES:
; NAME/KEY: rep_origin
; LOCATION: (655)..(1263)
; OTHER INFORMATION: Origin of replication ori ColeI
; FEATURES:
; NAME/KEY: gene
; LOCATION: (1264)..(2603)
; OTHER INFORMATION: NPT III gene coding for neomycin
; OTHER INFORMATION: phosphotransferase and kanamycinin resistance
; FEATURES:
; NAME/KEY: misc feature
; LOCATION: (2604)..(4098)
; OTHER INFORMATION: trfA locus from RK2 coding for two proteins, P285
; OTHER INFORMATION: and p382, enabling the increase of the rate of
; OTHER INFORMATION: replication
; FEATURES:
; NAME/KEY: misc feature
; LOCATION: (4106)..(4271)
; OTHER INFORMATION: T-DNA left border
; FEATURES:
; NAME/KEY: terminator
; LOCATION: (4272)..(4559)
; OTHER INFORMATION: No. US20030175976Alaline synthetase terminator
; FEATURES:
; NAME/KEY: gene
; LOCATION: (4575)..(5150)
; OTHER INFORMATION: Bar gene coding for phosphinotricin
; OTHER INFORMATION: acetyltransferase and herbicide resistance
; FEATURES:
; NAME/KEY: promoter
; LOCATION: (5150)..(5368)
; OTHER INFORMATION: No. US20030175976Alaline synthetase promoter
; FEATURES:
; NAME/KEY: misc feature
; LOCATION: (5368)..(5434)
; OTHER INFORMATION: MCS multiple cloning site
; FEATURES:
; NAME/KEY: misc feature
; LOCATION: (5434)..(5607)
; OTHER INFORMATION: T-DNA right border
; US-09-845-064-16

Query Match 94.3%; Score 4531.4; DB 10; Length 5614;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4532; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCGGGCTGGTTGCCCTCGCCGCTGGGCTGGCGCGCTATGGCCCTGCAACGCGCAG 60
Db 1 CCGGGCTGGTTGCCCTCGCCGCTGGGCTGGCGCGCTATGGCCCTGCAACGCGCAG 60

Qy 61 AAACCGCGTGAAGCCGTTGTCGAGACACCCGCGCGCGCGGCTGTGGATACCTCGCGG 120
Db 61 AAACCGCGTGAAGCCGTTGTCGAGACACCCGCGCGCGCGGCTGTGGATACCTCGCGG 120

Qy 121 AAAACTTGGCCCTCACTGACAGATAGAGGGCGGACGTTGACACTTGAGGGGCCGACTCAC 180
Db 121 AAAACTTGGCCCTCACTGACAGATAGAGGGCGGACGTTGACACTTGAGGGGCCGACTCAC 180

Qy 181 CCGCGCGGCGTTGACAGATGAGGGCGAGGCTCGATTTCCGCGCGCGACGTTGAGCTGGC 240
Db 181 CCGCGCGGCGTTGACAGATGAGGGCGAGGCTCGATTTCCGCGCGCGACGTTGAGCTGGC 240

Qy 241 CAGCCTCGCAATCGGCGAAACCGCTGATTTTACGCGAGTTTCCACAGATGATGTGA 300
Db 241 CAGCCTCGCAATCGGCGAAACCGCTGATTTTACGCGAGTTTCCACAGATGATGTGA 300

Qy 301 CAACGCTGGGATTAAGTCCCTCGCGTATTGACACTTGAGGGGGCGGACTACTGACAGAT 360
Db 301 CAACGCTGGGATTAAGTCCCTCGCGTATTGACACTTGAGGGGGCGGACTACTGACAGAT 360

Qy 361 GAGGGCGCGATCCTTGACACTTGAGGGCGAGAGTGCTGACAGATGAGGGCGCACCTAT 420

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Db 1501 GGGCAAAAGCAATAAACTTGCATGCACTAATGCTTGAAGCCAGGACAAATAACCTTATAG 1560  
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Db 1561 CTTGTAAATTTCTACCAAAATTTGGTTTCAAAATTCGGCTCCGTCGATACCTATGTTATACG 1620  
Qy 1621 CCACTTTTGAAGAACAACTTTGAAAGAGCTGTTTCTGGTATTTAAAGTTTGAAGTCAA 1680  
Db 1621 CCACTTTTGAAGAACAACTTTGAAAGAGCTGTTTCTGGTATTTAAAGTTTGAAGTCAA 1680  
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Db 1861 TAACTGGTGGGAGAAAATGAAAACCTTATATTTAAATAACAGCAGACCGCGGTATAAGG 1920  
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Db 2161 TACGAATAGCTTAGACAGCGCTTAGCCGAATTTGGATTTGATTACTTAAGTAAACGATCTGC 2220  
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Db 2281 TGAATTTTAAAGACGGAAAGCCCGAAGAGAACTTTGCTTTTCCACGCGCACTGGG 2340  
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Qy 2461 CGGGGAAGAACAGTATGTCAGCTATTTTGTGATTTTGTACTTACTGGGATCAAGCCTGATTTGGGA 2520  
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Qy 3001 AGCAAGCTACGGCAAGATCGAGCGGACAGCGTGCAACTGGCTCCGCTGCGCTGCGCG 3060  
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Qy 3301 GAGCGATGCCAACGACACGCGCGCTTGCCTGCTTCCACGCGCAACCAAGAAATCC 3360  
Db 3301 GAGCGATGCCAACGACACGCGCGCTTGCCTGCTTCCACGCGCAACCAAGAAATCC 3360  
Qy 3361 CGCGGAGCGCTGCAAAACAAAGTCAATTTCCACGTCAAAGGACGTTGAAGATCACCT 3420  
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Qy 3421 ACACCGGCTGAGCTGCGGGCGGACGATGAAGAACTGCTGAGGAGGAGGTTTGGAGT 3480  
Db 3421 ACACCGGCTGAGCTGCGGGCGGACGATGAAGAACTGCTGAGGAGGAGGTTTGGAGT 3480  
Qy 3481 AGCGAAGCGCACCCCTATCGGCGAGCCGATCACCTTCTACGAGCTTTTGCAGG 3540  
Db 3481 AGCGAAGCGCACCCCTATCGGCGAGCCGATCACCTTCTACGAGCTTTTGCAGG 3540  
Qy 3541 ACCTGGCTGGTTCGATCAATGCGCGGTAACAAGAGGCGGAGGAAATGCTTGCAGG 3600  
Db 3541 ACCTGGCTGGTTCGATCAATGCGCGGTAACAAGAGGCGGAGGAAATGCTTGCAGG 3600  
Qy 3601 TACAGCGACGCGGATGGGCTTCACTCCGACCGGCTTGGGCACTTGGAAATCGGTGTCG 3660  
Db 3601 TACAGCGACGCGGATGGGCTTCACTCCGACCGGCTTGGGCACTTGGAAATCGGTGTCG 3660

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Qy 3661 TGCTGCACCGCTTCCGGCTCCTCGACCGTGGCAAGAAACGTCCTCCGTTGCCAGGCTCTGA 3720
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Qy 3721 TCACGAGGAAATCGTCTGCTGCTGTTTCTCGCCAGCACTACACGAAATTCATATGGGAGA 3780
Db 3721 TCACGAGGAAATCGTCTGCTGCTGTTTCTCGCCAGCACTACACGAAATTCATATGGGAGA 3780
Qy 3781 AGTACCGCAAGCTGTGCCCGACCGCCGACGAGTGTTCGACTATTTTCAGCTCCGACCGGG 3840
Db 3781 AGTACCGCAAGCTGTGCCCGACCGCCGACGAGTGTTCGACTATTTTCAGCTCCGACCGGG 3840
Qy 3841 AGCGTACCGCTCAAGCTGGAACCTTCGCGCTCATGTGCGGATCGGATTCACCCGCG 3900
Db 3841 AGCGTACCGCTCAAGCTGGAACCTTCGCGCTCATGTGCGGATCGGATTCACCCGCG 3900
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Qy 4021 CAGTTCGGCTGGGGTTACGACGAGCGCTTTACTGGCATTTCTAGGTTGACGCTTT 4080
Db 4021 CAGTTCGGCTGGGGTTACGACGAGCGCTTTACTGGCATTTCTAGGTTGACGCTTT 4080
Qy 4081 CTGATGGGCTGCCTGTATCAGTGTGATTTTGTGCGAGCTGCGGCTCGGGAGCTGTT 4140
Db 4081 CTGATGGGCTGCCTGTATCAGTGTGATTTTGTGCGAGCTGCGGCTCGGGAGCTGTT 4140
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Db 4261 ATCTAGTAACATATGACCGCGCGATATTTTCTAGTTTGGCGCTATATTG 4320
Qy 4321 TTTTCTATCGCGTATTAATGTATATTTGCGGACTCTAATCATATAAAACCCATCTCAT 4380
Db 4321 TTTTCTATCGCGTATTAATGTATATTTGCGGACTCTAATCATATAAAACCCATCTCAT 4380
Qy 4381 AATACGCTATGCAATTACATGTTAATTTATACATGCTTAACGTAATTCACAGAAATAT 4440
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Db 4441 ATGATAATCATCGCAAGCGGCAAGAGGATTCATCTTAAGAACTTTATTGCAAAATG 4500
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Db 4501 TTTGAACGATCGTTTCGTGCGAGCTATGGGCCCTA 4533
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; Sequence 3, Application US/09845064
; Publication No. US20030175976A1
; GENERAL INFORMATION:
; APPLICANT: MERISTEM THERAPEUTICS
; TITLE OF INVENTION: CLEAN SYNTHETIC VECTORS, PLASMIDS, TRANSGENIC PLANTS
; TITLE OF INVENTION: AND PLANT PARTS CONTAINING SAID VECTORS, AND THEIR
; TITLE OF INVENTION: METHODS OF PRODUCTION
; FILE REFERENCE: SynVec1
; CURRENT APPLICATION NUMBER: US/09/845,064
; CURRENT FILING DATE: 2001-04-27
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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 5971
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Plasmid
; OTHER INFORMATION: pmrI118
; FEATURE:
; NAME/KEY: rep_origin
; LOCATION: (1)..(654)
; OTHER INFORMATION: Origin of replication ori RK2
; FEATURE:
; NAME/KEY: rep_origin
; LOCATION: (655)..(1263)
; OTHER INFORMATION: Origin of replication ori ColEI
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1264)..(2603)
; OTHER INFORMATION: NPT III gene coding for neomycin
; OTHER INFORMATION: phosphotransferase and kanamycin resistance
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2604)..(4098)
; OTHER INFORMATION: TrfA locus from pRK2 coding for two proteins,
; OTHER INFORMATION: P285 and P382, enabling the increase in the rate
; OTHER INFORMATION: of replication
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4106)..(4271)
; OTHER INFORMATION: T-DNA left border
; FEATURE:
; NAME/KEY: terminator
; LOCATION: (4272)..(4559)
; OTHER INFORMATION: No. US20030175976A1alaline synthetase terminator
; FEATURE:
; NAME/KEY: gene
; LOCATION: (4560)..(5556)
; OTHER INFORMATION: NPT II gene coding for neomycin phosphotransferase
; OTHER INFORMATION: and kanamycin resistance
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (5557)..(5770)
; OTHER INFORMATION: No. US20030175976A1alaline synthetase promoter
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (5791)..(5964)
; OTHER INFORMATION: T-DNA right border
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (5770)..(5791)
; OTHER INFORMATION: MCS multiple cloning site
; US-09-845-064-3
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Query Match 94.3%; Score 4531.4; DB 10; Length 5971;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4532; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 CCGGGCTGGTTGCCCTCGCGCTGGGCTGGCGCGCGCTCTATGGCCCTGCAAAACGCGCCAG 60
Db 1 CCGGGCTGGTTGCCCTCGCGCTGGGCTGGCGCGCGCTCTATGGCCCTGCAAAACGCGCCAG 60
Qy 61 AAACGCGCTCGAAGCCGTTGTGCAGACACCGCGCGCGCGCTGTGTGGATACCTCCGG 120
Db 61 AAACGCGCTCGAAGCCGTTGTGCAGACACCGCGCGCGCGCTGTGTGGATACCTCCGG 120
Qy 121 AAAACTTGGCCCTCACTGACAGATGAGGGCGGACGTTGACACTTGAGGGGCCGACTCAC 180
Db 121 AAAACTTGGCCCTCACTGACAGATGAGGGCGGACGTTGACACTTGAGGGGCCGACTCAC 180
Qy 181 CCGGCGCGCGCTTGACAGATGAGGGCGGACGCTCGATTTCGGCGCGCGACGTTGGAGCTGGC 240
Db 181 CCGGCGCGCGCTTGACAGATGAGGGCGGACGCTCGATTTCGGCGCGCGACGTTGGAGCTGGC 240
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DB	181	CGGCGCGCGCTTGACAGATCAGGGGCAGGCTCGATTTTCGGCCGGCAGCTGGAGCTGGC	240
QY	241	CAGCCTCGCAAAATCGGGAAACCCCTGATTTTATACGCGAGTTTCCCAAGATGATGTGGA	300
DB	241	CAGCCTCGCAAAATCGGGAAACCCCTGATTTTACGCGAGTTTCCCAAGATGATGTGGA	300
QY	301	CAAGCCTGGGATAAAGTGCCCTGCGGTATTGACACTTTGAGGGGCGCACTACTGACAGAT	360
DB	301	CAAGCCTGGGATAAAGTGCCCTGCGGTATTGACACTTTGAGGGGCGCACTACTGACAGAT	360
QY	361	GAGGGGCGCATCTTGACACTTCAGGGGCAAGTGCTGACAGATGAGGGGCGCACCTAT	420
DB	361	GAGGGGCGCATCTTGACACTTCAGGGGCAAGTGCTGACAGATGAGGGGCGCACCTAT	420
QY	421	TGACATTTGAGGGCTGTCCACAGGCAGAAATCCAGCATTTGCAAGGGTTTCCGCCCGT	480
DB	421	TGACATTTGAGGGCTGTCCACAGGCAGAAATCCAGCATTTGCAAGGGTTTCCGCCCGT	480
QY	481	TTTTTCGGCCACCGCTAACCTGTCTTTTAAACCTGCTTTTAAACCAATATTTATAACCTTG	540
DB	481	TTTTTCGGCCACCGCTAACCTGTCTTTTAAACCTGCTTTTAAACCAATATTTATAACCTTG	540
QY	541	TTTTTAAACAGGGCTGCGCCCTGTGCGGTGACCGCACGCCGAAAGGGGGTGCSCCCC	600
DB	541	TTTTTAAACAGGGCTGCGCCCTGTGCGGTGACCGCACGCCGAAAGGGGGTGCSCCCC	600
QY	601	CTTCTGAAACCTCCCGAAAGGTATGCGGTGTAATAACCGCACAGATGCGTAAGGAGA	660
DB	601	CTTCTGAAACCTCCCGAAAGGTATGCGGTGTAATAACCGCACAGATGCGTAAGGAGA	660
QY	661	AAATACCGCATCAGGGCTCTTTCGGCTTCCTCGCTCATCTGACTCGCTGCGTCTGGTCT	720
DB	661	AAATACCGCATCAGGGCTCTTTCGGCTTCCTCGCTCATCTGACTCGCTGCGTCTGGTCT	720
QY	721	CGGCTGGGCGAGCGGTATCAGCTCACTCAAAGGCGTAAATACGGTTATCCACAGATCA	780
DB	721	CGGCTGGGCGAGCGGTATCAGCTCACTCAAAGGCGTAAATACGGTTATCCACAGATCA	780
QY	781	GGGGATAACGAGGAAAGAAACATGTAGCAAAAGCCAGCAAAAGGCCAGGAAACCGTAAA	840
DB	781	GGGGATAACGAGGAAAGAAACATGTAGCAAAAGCCAGCAAAAGGCCAGGAAACCGTAAA	840
QY	841	AAGCGCGGTGCTGGCGTTTTTTCATAGGCTCGCCCCCTGTACGAGCATCAAAAAT	900
DB	841	AAGCGCGGTGCTGGCGTTTTTTCATAGGCTCGCCCCCTGTACGAGCATCAAAAAT	900
QY	901	CGACGCTCAGTCAGAGTGGCGAAACCCGACGAGCTATAAGATACCAAGGGTTTCCC	960
DB	901	CGACGCTCAGTCAGAGTGGCGAAACCCGACGAGCTATAAGATACCAAGGGTTTCCC	960
QY	961	CCTGGAAGCTCCCTGTCGCTCTCTGTTCCGACCTGCGCTTACCGGATACCTGTCC	1020
DB	961	CCTGGAAGCTCCCTGTCGCTCTCTGTTCCGACCTGCGCTTACCGGATACCTGTCC	1020
QY	1021	GCCTTTTCTCCCTTCGGGAAGCGTGCGCTTCTCATAGCTCAGCGTGAAGTATCTCAGT	1080
DB	1021	GCCTTTTCTCCCTTCGGGAAGCGTGCGCTTCTCATAGCTCAGCGTGAAGTATCTCAGT	1080
QY	1081	TCGSGTGAAGTTCGTTCCGCTCCAGCTGGGCTGTGTGACGAAACCCCGCTTCAGCCGAC	1140
DB	1081	TCGSGTGAAGTTCGTTCCGCTCCAGCTGGGCTGTGTGACGAAACCCCGCTTCAGCCGAC	1140
QY	1141	CGCTGCGCTTATCCGGTAACTATCGTCTTTGAGTCCAAACCCGGTAAAGACGACTTATCG	1200
DB	1141	CGCTGCGCTTATCCGGTAACTATCGTCTTTGAGTCCAAACCCGGTAAAGACGACTTATCG	1200
QY	1201	CCACTGCGAGCAGCTTCTACCAATAATCCGCGATAAACCCAGCGAAACCTTTGAGGTGAT	1260
DB	1201	CCACTGCGAGCAGCTTCTACCAATAATCCGCGATAAACCCAGCGAAACCTTTGAGGTGAT	1260
QY	1261	AGGTAAGATTATACCGAGGTATGAAACAGAGAAATTTGACCTTTACAGAAATCTCTATGA	1320
DB	1261	AGGTAAGATTATACCGAGGTATGAAACAGAGAAATTTGACCTTTACAGAAATCTCTATGA	1320

Qy		1321	AGGCCATATTTAAAAAGCTCAACAACGAAAGAGGATGAAGAGGATGAGAGGCAGATTG	1380
Db		1321	AGGCCATATTTAAAAAGCTACCAAGACGAAAGAGGATGAAGAGGATGAGAGGCAGATTG	1380
Qy		1381	CCTTGAATATATTGACAAATACTCATAGATAAATACATCTTTTTATAGAAGATATCGCCG	1440
Db		1381	CCTTGAATATATTGACAAATACTCATAGATAAATACATCTTTTTATAGAAGATATCGCCG	1440
Qy		1441	TATGTAAAGGATTTTCAGGGGCAAGGCATAGCAGCGCTTATCAATATATCTATAGAAT	1500
Db		1441	TATGTAAAGGATTTTCAGGGGCAAGGCATAGCAGCGCTTATCAATATATCTATAGAAT	1500
Qy		1501	GGGCAAGCATAAAACTTCGATGGACTAATGCTTGAAACCAGGACAATAAACCTTATAG	1560
Db		1501	GGGCAAGCATAAAACTTCGATGGACTAATGCTTGAAACCAGGACAATAAACCTTATAG	1560
Qy		1561	CTTGTAATTTCTACCAAAATTTGTGGTTTCAAATCGCTCGATCTATGTTATACG	1620
Db		1561	CTTGTAATTTCTACCAAAATTTGTGGTTTCAAATCGCTCGATCTATGTTATACG	1620
Qy		1621	CCAACCTTTGAAAACAACTTTGAAAAAGCTGTTTTCTGGTATTTAAGGTTTTAGAAATGCAA	1680
Db		1621	CCAACCTTTGAAAACAACTTTGAAAAAGCTGTTTTCTGGTATTTAAGGTTTTAGAAATGCAA	1680
Qy		1681	GGAACAGTGAATTTGGAGTTGCTTGTATAAATTAGCTTCTTGGGTATCTTTAAATACT	1740
Db		1681	GGAACAGTGAATTTGGAGTTGCTTGTATAAATTAGCTTCTTGGGTATCTTTAAATACT	1740
Qy		1741	GTAGAAAAGAGGAAGAAATAATAATGGCTAAAAATGAGAAATCACCGGAAATTGAAAAA	1800
Db		1741	GTAGAAAAGAGGAAGAAATAATAATGGCTAAAAATGAGAAATCACCGGAAATTGAAAAA	1800
Qy		1801	ACTGATCGAAAAATAACGCTGCGTAAAGATACGGAAGGAATCTCTCTCTAAGGPTATA	1860
Db		1801	ACTGATCGAAAAATAACGCTGCGTAAAGATACGGAAGGAATCTCTCTCTAAGGPTATA	1860
Qy		1861	TAAGCTGGTGGGAGAAAATGAAAACCTATATTTAAAAATGACGGACAGCGGTATAAAGG	1920
Db		1861	TAAGCTGGTGGGAGAAAATGAAAACCTATATTTAAAAATGACGGACAGCGGTATAAAGG	1920
Qy		1921	GACCACCTATGATGTGGAAACGGAAAAAGGACATGATGCTATGGCTGGAAGAAAGCTGCC	1980
Db		1921	GACCACCTATGATGTGGAAACGGAAAAAGGACATGATGCTATGGCTGGAAGAAAGCTGCC	1980
Qy		1981	TGTTCCMAAGGTCTGCACTTTGAAACGGCATGATGCTGGAGCAATCTGCTCATGAGTGA	2040
Db		1981	TGTTCCMAAGGTCTGCACTTTGAAACGGCATGATGCTGGAGCAATCTGCTCATGAGTGA	2040
Qy		2041	GGCCGATGGCGTCTTTGCTCGGAAGATGAAGATGAACAAAGCCCTGAAAAGATTAT	2100
Db		2041	GGCCGATGGCGTCTTTGCTCGGAAGATGAAGATGAACAAAGCCCTGAAAAGATTAT	2100
Qy		2101	CGAGCTGTATGCGGAGTGATCAGGCTCTTTCACTCCATCGACATATCGGATTTGCCCTA	2160
Db		2101	CGAGCTGTATGCGGAGTGATCAGGCTCTTTCACTCCATCGACATATCGGATTTGCCCTA	2160
Qy		2161	TACGAATAGCTTAGACAGCGGCTTTAGCCGNAATTTGGATTACTTACTGNAATACCATCTGCC	2220
Db		2161	TACGAATAGCTTAGACAGCGGCTTTAGCCGNAATTTGGATTACTTACTGNAATACCATCTGCC	2220
Qy		2221	CGATGTGGATTGCAAAACTGGGAAGACACTCCATTTAAAGATCCGCGCAGCTGTA	2280
Db		2221	CGATGTGGATTGCAAAACTGGGAAGACACTCCATTTAAAGATCCGCGCAGCTGTA	2280
Qy		2281	TGATTTTTTAAAGACGAAAAAGCCCAGAGGAACCTTGCTTTTCCACGGCGACCTGGG	2340
Db		2281	TGATTTTTTAAAGACGAAAAAGCCCAGAGGAACCTTGCTTTTCCACGGCGACCTGGG	2340
Qy		2341	AGACAGCAACTCTTTGTGNAAGATGGCAAGTAAGTGGCTTTATTGATCTTTGGGAGNAG	2400
Db		2341	AGACAGCAACTCTTTGTGNAAGATGGCAAGTAAGTGGCTTTATTGATCTTTGGGAGNAG	2400

Qy	2401	CGCAGGGCGGCAAGTGGTATGACATTGGCTTCTCGGTCCGGTCCGATCAGGAGGATAT	2460
Db	2401		
Qy	2461	CGGGAAGAAACAGTATGTCAGAGCTATTTTTTGACTTACTGGGGATCAAGCCTGATTGGGA	2520
Db	2461		
Qy	2521	GAAAAATAAATAATATATTTTATCTGGATGAATTTGTTTTAGTACTTACTGGGATCAAGCCTGATTGGGA	2580
Db	2521		
Qy	2581	ATGCGGCGACAGCAGGCGCACCGACTTCTTCCGCATCAAGTGTTTTGGCTCTCAGG	2640
Db	2581		
Qy	2641	CCGAGGCCCAAGTATTTTGGGCAAGGGTCCGCTGGTATTCGTCAGGCGCAAGATTC	2700
Db	2641		
Qy	2701	GGAATACAAAGTACGAGAGACGGCCAGACGGTCTACGGGACCGAATTCAATTGGCCGATA	2760
Db	2701		
Qy	2761	AGGTGGATTATCTGGACACCAAGGCACAGCGGCTCAAAATCAGGAATAAGGGCACATTG	2820
Db	2761		
Qy	2821	CCC CGGCGT GAGTCGGGCGCAATCCCGCAAGAGGGTGAATGAATCGGACGTTTGACCGGA	2880
Db	2821		
Qy	2881	AGGCATACAGCAAGAACTGATCGACCGGGTTTTCCGCGAGGATGCCGAAACCATCG	2940
Db	2881		
Qy	2941	CNAGCCGACGTCATCGGTGCGCCCGCGAAACCTTCCAGTCCGTCGGTCCGATGTC	3000
Db	2941		
Qy	3001	AGCAAGCTAGCGGCAAGATCGAGCGCACAGCGTGCAACTGGCTCCCGCTGCCCTGCCCG	3060
Db	3001		
Qy	3061	CGCCATCGGCGCGTGGAGCGTTTCGCGTCTCGAAACAGGAGCGCGAGTTTGGCGA	3120
Db	3061		
Qy	3121	AGTCGATGACCATCGACCGGAGAACTATGACGACCAAGAGCGAAACCGCGCGC	3180
Db	3121		
Qy	3181	AGGACCTGGCAAAACAGCTCAGCGAGGCGCAAGCGCGCGCTTCTGAAAACACACGAAGC	3240
Db	3181		
Qy	3241	AGCAGATCAAGAAATGACGCTTTCCTTTGTCGATATTTGCGCCGTGGCGGACACGATGC	3300
Db	3241		
Qy	3301	GAGCGATGCCAAACGACAGCGCCGCTCTGCCCTGTTCACCGCGCAACAAGAAATCC	3360
Db	3301		
Qy	3361	CGCGAGGGCGCTGCAAAAACAAAGTCAATTTTCCACGTCAACAAAGGACGTGAAGATCACCT	3420
Db	3361		
Qy	3421	ACACCGGCTCGAGCTGGGCGGACGATGACGAACTGGTGTGGCAGCAGGTGTGGAGT	3480
Db	3421		
Qy	3481	ACGGAAGCGCACCCCTATCGGCGAGCGGATCACCTTTCACGCTTCTACGAGCTTTGCCAGG	3540
Db	3481		

Db	3481	ACGGAAGCGCACCCCTATCGGCGAGCGGATCACCTTTCACGCTTCTACGAGCTTTGCCAGG	3540
Qy	3541	ACCTGGGCTGGTGCATCAATAGCCGGTATTAACGAAGGCCGAGGAATGCCTGTTCGGCC	3600
Db	3541		
Qy	3601	TACAGCGAGCGGATGGGCTTACGTCGACCGCGTGGCAACCTTGGCACTTGGAAATCGGTGTCG	3660
Db	3601		
Qy	3661	TGCTGCACCGCTTCCCGCTCCTGGACCGTGGCAAGAAACCTCCCGTTTGCAGGCTCTGA	3720
Db	3661		
Qy	3721	TCGACGAGAAATCGTGGTGTCTGCTGCTGCTGCTGGCGACCACTACAGAAATTCATATGGGAG	3780
Db	3721		
Qy	3781	AGTACCGCAAGCTGTCGCGGACCGGCGGAGGATGTTTCGACTATTTTCAGCTCGCACCGG	3840
Db	3781		
Qy	3841	AGCGGTACCCGCTCAAGCTGGAAACCTTCGCGCTCATGTGCGGATCGGATTCACCCGCG	3900
Db	3841		
Qy	3901	TGAAGAAGTGGCGGAGGAGTGGCGAAAGCTTCGCAAGAGTTTGCAGGCGAGCGGCTGG	3960
Db	3901		
Qy	3961	TGAAACACCGCTGGGCTCAATGATGACCTGGTGCATTCGAAACCTAGGCGCTTGTGGGT	4020
Db	3961		
Qy	4021	CAGTTCGGCTGGGGTTCAGCAGCAGCGCTTTTACTTGGCATTTCTAGGTTCAGCTCTT	4080
Db	4021		
Qy	4081	CTGATGGGCTGCTGTATCAGTGGTGTATTTTGTGCGGAGCTCCCGTTCGGGAGCTGTT	4140
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Qy	4141	GGCTGGCTGGCGAGGATATTTGGTGTAAACAAATTTAGCGCTTAGACAATTAATA	4200
Db	4141		
Qy	4201	ACACATTTGCGGAGCTTTTAAATGACTGGGGCTATCCCGGGGGATATCCATAGGCCCG	4260
Db	4201		
Qy	4261	ATCTAGTAACATTAATGACACCGCGCGGATAATTTATCTTAGTTTGGCGCTATATTTTG	4320
Db	4261		
Qy	4321	TTTTCTATCGCGTATTAATGATATTTGCGGACTCTAATCATATAAAACCCATCTCAT	4380
Db	4321		
Qy	4381	AATAAGCTCATGCAATACATGTTTAAATTTATTTACATGCTTAAACGTAATTCACAGAAATAT	4440
Db	4381		
Qy	4441	ATGATTAATCATCGGAGACCGGCAACAGGATTCGAACTTTAAGAACTTTATTTGCCAAATG	4500
Db	4441		
Qy	4501	TTTGAACGATCGTTCGTCGAGCTATGGGCCGA 4533	
Db	4501		

US-09-845-064-4  
; Sequence 4, Application US/09845064  
; Publication No. US20030175976A1  
; GENERAL INFORMATION:  
; APPLICANT: MERISTEM THERAPEUTICS  
; TITLE OF INVENTION: CLEAN SYNTHETIC VECTORS, PLASMIDS, TRANSGENIC PLANTS  
; TITLE OF INVENTION: AND PLANT PARTS CONTAINING SAID VECTORS, AND THEIR  
; TITLE OF INVENTION: METHODS OF PRODUCTION  
; FILE REFERENCE: Synvec1  
; CURRENT APPLICATION NUMBER: US/09/845,064  
; CURRENT FILING DATE: 2001-04-27  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: Patentin ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 6016  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Plasmid  
; OTHER INFORMATION: pMRT1119  
; FEATURE:  
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; LOCATION: (1)-(654)  
; OTHER INFORMATION: Origin of replication ori RK2  
; FEATURE:  
; NAME/KEY: rep origin  
; LOCATION: (655)..(1263)  
; OTHER INFORMATION: Origin of replication ori ColEI  
; FEATURE:  
; NAME/KEY: gene  
; LOCATION: (1264)..(2603)  
; OTHER INFORMATION: NPT III gene coding for neomycin  
; OTHER INFORMATION: phosphotransferase and kanamycin resistance  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (2604)..(4098)  
; OTHER INFORMATION: TrfA locus coding for two proteins, P285 and P382,  
; OTHER INFORMATION: enabling the increase in the rate of replication  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (4106)..(4271)  
; OTHER INFORMATION: T-DNA left border  
; FEATURE:  
; NAME/KEY: terminator  
; LOCATION: (4272)..(4559)  
; OTHER INFORMATION: No. US20030175976A1: alaine synthetase terminator  
; FEATURE:  
; NAME/KEY: gene  
; LOCATION: (4560)..(5556)  
; OTHER INFORMATION: NPT II gene coding for neomycin phosphotransferase  
; OTHER INFORMATION: and kanamycin resistance  
; FEATURE:  
; NAME/KEY: promoter  
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; OTHER INFORMATION: No. US20030175976A1: alaine synthetase promoter  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (5836)..(6009)  
; OTHER INFORMATION: T-DNA right border  
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; NAME/KEY: misc feature  
; LOCATION: (5770)..(5836)  
; OTHER INFORMATION: MCS multiple cloning site  
US-09-845-064-4

Query Match 94.3%; Score 4531.4; DB 10; Length 6016;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 4532; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCGGGCTGGTTCCTCGCGCTGGGCTGGGCGCGCTATGCGCCCTGCAAAACGCCGCGAG 60  
Db 1 CCGGGCTGGTTCCTCGCGCTGGGCTGGGCGCGCTATGCGCCCTGCAAAACGCCGCGAG 60

61 AAACGCCGTGAAAGCCGTGTGCGAGACACCGCGCGCGCGCGCTTTGTGGATACCTCGCGG 120  
Db AAACGCCGTGAAAGCCGTGTGCGAGACACCGCGCGCGCGCGCTTTGTGGATACCTCGCGG 120  
Qy 121 AAAAATTGGCCCTCACTGACAGATGAGGGCGAGCGCTTGACACTTGAGGGCGCGACTCAC 180  
Db 121 AAAAATTGGCCCTCACTGACAGATGAGGGCGAGCGCTTGACACTTGAGGGCGCGACTCAC 180  
Qy 181 CCGCGCGCGCTTGTGACAGATGAGGGCGAGCGCTCGATTTTCGGCGCGCGACCTGGAGCTGGC 240  
Db 181 CCGCGCGCGCTTGTGACAGATGAGGGCGAGCGCTCGATTTTCGGCGCGCGACCTGGAGCTGGC 240  
Qy 241 CAGCCTCGCAAAATCGCGGAAACCGCTGATTTTACCGGAGTTTCCACAGATGATGGA 300  
Db 241 CAGCCTCGCAAAATCGCGGAAACCGCTGATTTTACCGGAGTTTCCACAGATGATGGA 300  
Qy 301 CAAGCCTGGGGATAAGTGCCTCGGTATTGACACTTGAGGGCGCGACTACTGACAGAT 360  
Db 301 CAAGCCTGGGGATAAGTGCCTCGGTATTGACACTTGAGGGCGCGACTACTGACAGAT 360  
Qy 361 GAGGGCGCGGATCCTTTGACACTTTGAGGGCGAGAGTGTCTGACAGATGAGGGCGCGACTAT 420  
Db 361 GAGGGCGCGGATCCTTTGACACTTTGAGGGCGAGAGTGTCTGACAGATGAGGGCGCGACTAT 420  
Qy 421 TGACATTTGAGGGCTGTCCACAGGAGAAATCCAGCATTTTCAAGGGTTTCGCGCGT 480  
Db 421 TGACATTTGAGGGCTGTCCACAGGAGAAATCCAGCATTTTCAAGGGTTTCGCGCGT 480  
Qy 481 TTTTCGGCCACCGCTAACCTGTCTTTAACTGCTTTTAAACCAATATTTATAACCTTG 540  
Db 481 TTTTCGGCCACCGCTAACCTGTCTTTAACTGCTTTTAAACCAATATTTATAACCTTG 540  
Qy 541 TTTTAAACAGGGCTGCGCGCTGTGCGCGTACCGCGCACCGCGAAGGGGGTTCGCCCC 600  
Db 541 TTTTAAACAGGGCTGCGCGCTGTGCGCGTACCGCGCACCGCGAAGGGGGTTCGCCCC 600  
Qy 601 CTTCTCGAACCTTCCCGAAGATATGCGGTGTGAAATACCGCACAGATGCGTAAGAGA 660  
Db 601 CTTCTCGAACCTTCCCGAAGATATGCGGTGTGAAATACCGCACAGATGCGTAAGAGA 660  
Qy 661 AATACGGATCAGGGCTCTTCCGCTTCTCGCTCACTGACTCGCTCGCTCGCTCGT 720  
Db 661 AATACGGATCAGGGCTCTTCCGCTTCTCGCTCACTGACTCGCTCGCTCGCTCGT 720  
Qy 721 CGCTCGCGAGCGGTATCAGCTCACTCAAAGCGGTAAATACGTTATCCACAGATCA 780  
Db 721 CGCTCGCGAGCGGTATCAGCTCACTCAAAGCGGTAAATACGTTATCCACAGATCA 780  
Qy 781 GGGGATAACCGAGGAAAGAACATGTGAGCAAAAGCCAGCAAAAGCCAGGAAACCGTAAA 840  
Db 781 GGGGATAACCGAGGAAAGAACATGTGAGCAAAAGCCAGCAAAAGCCAGGAAACCGTAAA 840  
Qy 841 AAGGCCGCTTGTGCGCTTTTCCATAGGCTCCGCGCGCTCGCTCGCTCGCTCGCT 900  
Db 841 AAGGCCGCTTGTGCGCTTTTCCATAGGCTCCGCGCGCTCGCTCGCTCGCTCGCT 900  
Qy 901 CGACGCTCAAGTCAGAGTGGCGAAACCCGACAGGACTATAAGATACCAAGGGGTTTCCC 960  
Db 901 CGACGCTCAAGTCAGAGTGGCGAAACCCGACAGGACTATAAGATACCAAGGGGTTTCCC 960  
Qy 961 CTTGGAAGCTTCCCTCGCTCGCTTCTCTGTTCCGACCTTCCGCTTACCGGATACCTGTCC 1020  
Db 961 CTTGGAAGCTTCCCTCGCTCGCTTCTCTGTTCCGACCTTCCGCTTACCGGATACCTGTCC 1020  
Qy 1021 GCCTTTCTCCCTTCGGGAAAGCGTGGCGCTTCTCATAGCTCAGCTGATAGGTATCTCAGT 1080  
Db 1021 GCCTTTCTCCCTTCGGGAAAGCGTGGCGCTTCTCATAGCTCAGCTGATAGGTATCTCAGT 1080  
Qy 1081 TCGGTGTAGTGTCTCGCTCCAAGCTGGGCTGTGTGACAGAAACCCCGCTTACGCGGAC 1140  
Db 1081 TCGGTGTAGTGTCTCGCTCCAAGCTGGGCTGTGTGACAGAAACCCCGCTTACGCGGAC 1140  
Qy 1141 CGCTGCGCTTATCCGGTAACTATCGTCTTGAGTCCAAACCCCGGTAAGACAGACTTATCG 1200

Db	1141		CGCTGGCCCTTATCCGGTAACATACGTCCTTGGAGTCCAAACCCGGTAAGACACGACTTATCG	1200
Qy	1201		CCACTGGCAGAGCTTCTACATAATCCGGATATAAACCCAGCGAACCAATTTGAGGTGAT	1260
Db	1201		CCACTGGCAGAGCTTCTACATAATCCGGATATAAACCCAGCGAACCAATTTGAGGTGAT	1260
Qy	1261		AGGTAAAGATTATACCGAGGTATGAACACGAGAAATGGACCTTTACAGAAATTTACTCTATGA	1320
Db	1261		AGGTAAAGATTATACCGAGGTATGAACACGAGAAATGGACCTTTACAGAAATTTACTCTATGA	1320
Qy	1321		AGGCCCATATTTAAAAAGCTACCAAGACGAAGAGATGAAGAGGATGAGGAGGCGAGATTG	1380
Db	1321		AGGCCCATATTTAAAAAGCTACCAAGACGAAGAGATGAAGAGGATGAGGAGGCGAGATTG	1380
Qy	1381		CTTTGAAATATATTGACAATCTGATAAGATAATACATCTTTTATATAGAAAGATATCGCCG	1440
Db	1381		CTTTGAAATATATTGACAATCTGATAAGATAATACATCTTTTATATAGAAAGATATCGCCG	1440
Qy	1441		TATCTAAGGATTTTCAGGGGCAAGGCATAGCGAGCGCTTATCAATATATCTATAGAAT	1500
Db	1441		TATCTAAGGATTTTCAGGGGCAAGGCATAGCGAGCGCTTATCAATATATCTATAGAAT	1500
Qy	1501		GGGCAAAAGCATAAAACTTGCATGGACTAATGCTTTGAAACCCAGGACAAATAACCTTATAG	1560
Db	1501		GGGCAAAAGCATAAAACTTGCATGGACTAATGCTTTGAAACCCAGGACAAATAACCTTATAG	1560
Qy	1561		CTTTGAAATTTCTACCAAAATTTGGTTTCAAAATCGGCTCCGTCGATCTATGTTATACG	1620
Db	1561		CTTTGAAATTTCTACCAAAATTTGGTTTCAAAATCGGCTCCGTCGATCTATGTTATACG	1620
Qy	1621		CCAACTTTGAAACAACTTTGAAAGAGCTGTTTCTCGTATTTAAAGCTTTTAAAGTGAACAA	1680
Db	1621		CCAACTTTGAAACAACTTTGAAAGAGCTGTTTCTCGTATTTAAAGCTTTTAAAGTGAACAA	1680
Qy	1681		GGAACTGTAATTTGGAGTTCGTCTGTTTAAATTTAGCTTCTTGGGGTATCTTTAAATACT	1740
Db	1681		GGAACTGTAATTTGGAGTTCGTCTGTTTAAATTTAGCTTCTTGGGGTATCTTTAAATACT	1740
Qy	1741		GTAGAAAAGAGGAGGAAATAATAATGGCTTAAATGAGAAATATCAACCGAAATGAAAAA	1800
Db	1741		GTAGAAAAGAGGAGGAAATAATAATGGCTTAAATGAGAAATATCAACCGAAATGAAAAA	1800
Qy	1801		ACTGATCGAAAAATACCGCTCGTAAAGATACCGAGGAGTGTCTCTCGTAAAGGTATA	1860
Db	1801		ACTGATCGAAAAATACCGCTCGTAAAGATACCGAGGAGTGTCTCTCGTAAAGGTATA	1860
Qy	1861		TAACTGCTGGGAGAAAATGAAAAACCTATATTTAAAAATGACGACACCGCGTATAAAGG	1920
Db	1861		TAACTGCTGGGAGAAAATGAAAAACCTATATTTAAAAATGACGACACCGCGTATAAAGG	1920
Qy	1921		GACCACCTATGATGTGAAACGGGAAAAGGACATGATGCTATGGCTGGAAGGAAAGCTGCC	1980
Db	1921		GACCACCTATGATGTGAAACGGGAAAAGGACATGATGCTATGGCTGGAAGGAAAGCTGCC	1980
Qy	1981		TGTTCCAAAGGCTCTGCATTTGAACGCGATGAGTGGCTGGAGCAATCTGCTCATGAGTGA	2040
Db	1981		TGTTCCAAAGGCTCTGCATTTGAACGCGATGAGTGGCTGGAGCAATCTGCTCATGAGTGA	2040
Qy	2041		GGCCGATGGGCTCTTTGCTCGGAAGAGTATGAAGATGAACAAAGCCCTGAAAAAGATTAT	2100
Db	2041		GGCCGATGGGCTCTTTGCTCGGAAGAGTATGAAGATGAACAAAGCCCTGAAAAAGATTAT	2100
Qy	2101		CGAGCTGATTCGGAGTGCATCAGGCTCTTTCACTCCATCGACATATCGGATTTGCCCTA	2160
Db	2101		CGAGCTGATTCGGAGTGCATCAGGCTCTTTCACTCCATCGACATATCGGATTTGCCCTA	2160
Qy	2161		TACCAATAGCTTACACAGCGCTTAGCGGATTCGATTTACTTCTGTAATACGATCTGGC	2220
Db	2161		TACCAATAGCTTACACAGCGCTTAGCGGATTCGATTTACTTCTGTAATACGATCTGGC	2220
Qy	2221		CGATGTGGATTTGGAAAACTGGGAAGAGACACTCCATTTAAAGATCCGCGAGCTGTA	2280
Db	2221		CGATGTGGATTTGGAAAACTGGGAAGAGACACTCCATTTAAAGATCCGCGAGCTGTA	2280

Db	2221		CGATGTGGATTTGGAAAACTGGGAAGAGACACTCCATTTAAAGATCCGCGAGCTGTA	2280
Qy	2281		TGATTTTTTAAAGACGGAAAAGCCGAAGAGAACTTGTCTTTTCCACGGGACCTGGG	2340
Db	2281		TGATTTTTTAAAGACGGAAAAGCCGAAGAGAACTTGTCTTTTCCACGGGACCTGGG	2340
Qy	2341		AGACACAAACATCTTTTGTGAAAAGATGGCAAAGTAAGTGGCTTTATTTGATCTTGGGAGAAG	2400
Db	2341		AGACACAAACATCTTTTGTGAAAAGATGGCAAAGTAAGTGGCTTTATTTGATCTTGGGAGAAG	2400
Qy	2401		CGCAGGGCGGACAACTGCTGATGACATTTGCTGCTTCTCGGTCGGGTGATCAGGAGGATAT	2460
Db	2401		CGCAGGGCGGACAACTGCTGATGACATTTGCTGCTTCTCGGTCGGGTGATCAGGAGGATAT	2460
Qy	2461		CGGGGAGAACAGTATGTCAGACTATTTTGTGACTTACCTGGGATCAAGCTCATTTGGGA	2520
Db	2461		CGGGGAGAACAGTATGTCAGACTATTTTGTGACTTACCTGGGATCAAGCTCATTTGGGA	2520
Qy	2521		GAAAAATAAATAATTTACTGATGAAATTTGTTTACTACCTAGATGTGGCGCAACG	2580
Db	2521		GAAAAATAAATAATTTACTGATGAAATTTGTTTACTACCTAGATGTGGCGCAACG	2580
Qy	2581		ATGCCGGGACAAAGCAGGAGCGCACCGACTTCTTCCGCAATCAAGTGTTTGGCTCTCAGG	2640
Db	2581		ATGCCGGGACAAAGCAGGAGCGCACCGACTTCTTCCGCAATCAAGTGTTTGGCTCTCAGG	2640
Qy	2641		CCGAGGCCACCGCAAGTATTTGGGCAAGGGTTCGCTGTTATTTCTGTCAGGCGCAAGTTC	2700
Db	2641		CCGAGGCCACCGCAAGTATTTGGGCAAGGGTTCGCTGTTATTTCTGTCAGGCGCAAGTTC	2700
Qy	2701		GGAAATACCAAGTACGAGAAGGACGGCCAGACGGTCTTACGGGACCGACTTCTTATTTGCCGATA	2760
Db	2701		GGAAATACCAAGTACGAGAAGGACGGCCAGACGGTCTTACGGGACCGACTTCTTATTTGCCGATA	2760
Qy	2761		AGTGATATTTCTGGACACCAAGGACACAGGCGGGTCAAAATCAGGAATTAAGGCGACATTG	2820
Db	2761		AGTGATATTTCTGGACACCAAGGACACAGGCGGGTCAAAATCAGGAATTAAGGCGACATTG	2820
Qy	2821		CCCCGGCTGAGTCGGGGCAATCCCGCAAGGAGGTGAATGAATCGGACGCTTTGACCGGA	2880
Db	2821		CCCCGGCTGAGTCGGGGCAATCCCGCAAGGAGGTGAATGAATCGGACGCTTTGACCGGA	2880
Qy	2881		AGGCATACAGGCAAGAACTGATCGACCGCGGGTTTTCCGCGAGGATGCCGAAACCATCG	2940
Db	2881		AGGCATACAGGCAAGAACTGATCGACCGCGGGTTTTCCGCGAGGATGCCGAAACCATCG	2940
Qy	2941		CAAGCGCACCGTCATGCGTGGCGCCCGCGGAAACCTTCCAGTCCGTCGGCTCGATGGTCC	3000
Db	2941		CAAGCGCACCGTCATGCGTGGCGCCCGCGGAAACCTTCCAGTCCGTCGGCTCGATGGTCC	3000
Qy	3001		AGCAAGCTACGGCCAAAGATCGAGCGCAGACGCTGCAACTGGCTCCCTCGCTGCGCCG	3060
Db	3001		AGCAAGCTACGGCCAAAGATCGAGCGCAGACGCTGCAACTGGCTCCCTCGCTGCGCCG	3060
Qy	3061		CGCCATCGGCGCGCTGAGAGCGTTTCGCTGCTCTCGAAACAGGAGGCGGAGGTTTGGCGA	3120
Db	3061		CGCCATCGGCGCGCTGAGAGCGTTTCGCTGCTCTCGAAACAGGAGGCGGAGGTTTGGCGA	3120
Qy	3121		AGTCGATGACCATCGACACGCGAGGAATATATGACGACCAAGAGCGGAAAACCGCGGCG	3180
Db	3121		AGTCGATGACCATCGACACGCGAGGAATATATGACGACCAAGAGCGGAAAACCGCGGCG	3180
Qy	3181		AGGACCTGGCAAAACAGGTTCAGCGAGGCAAGCGCGCTTGTCTGAAACACACGAGAGC	3240
Db	3181		AGGACCTGGCAAAACAGGTTCAGCGAGGCAAGCGCGCTTGTCTGAAACACACGAGAGC	3240
Qy	3241		AGCAGATCAAGGAAATTCAGCTTTTCTTGTTCGATATTCGCGCTGGCGGACACGATGC	3300
Db	3241		AGCAGATCAAGGAAATTCAGCTTTTCTTGTTCGATATTCGCGCTGGCGGACACGATGC	3300
Qy	3301		GAGCGATGCCAAACGACACGCGCCGCTCTGCGCTGTTTCCACCGCGCAACAGAAATCC	3360
Db	3301		GAGCGATGCCAAACGACACGCGCCGCTCTGCGCTGTTTCCACCGCGCAACAGAAATCC	3360



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QY 3361 CGGCGAGGCGCTGCAAAACAAGGTCAATTTTCCACGTCACCAAGGACGTGAAGATCACCT 3420
Db 3361 CGGCGAGGCGCTGCAAAACAAGGTCAATTTTCCACGTCACCAAGGACGTGAAGATCACCT 3420
QY 3421 ACACCGGCTCGAGCTGCGGGCGGACGATACGAACTGGTGTGGCAGCAGGTGTGGAGT 3480
Db 3421 ACACCGGCTCGAGCTGCGGGCGGACGATACGAACTGGTGTGGCAGCAGGTGTGGAGT 3480
QY 3481 ACAGGAGCGCACCCCTATCGGCGAGCGCATCACTTTCAGCTTTCAGAGCTTTGCCAGG 3540
Db 3481 ACAGGAGCGCACCCCTATCGGCGAGCGCATCACTTTCAGCTTTCAGAGCTTTGCCAGG 3540
QY 3541 ACCTGGGCTGGTCAATCAATGGCGGTATTACAGAAAGGCGGAGGAATGCTCTCGCGCC 3600
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QY 3601 TACAGGCGACGGGATGGGCTTACGTCGACCGCTGGGACCGCTTGGGACCTGGGAATCGGTGCG 3660
Db 3601 TACAGGCGACGGGATGGGCTTACGTCGACCGCTGGGACCGCTTGGGACCTGGGAATCGGTGCG 3660
QY 3661 TGCTGACCGCTTCCGGCTCTCGACCGTGGCAAGAAACGTCCTCGTTCAGGTCCTGA 3720
Db 3661 TGCTGACCGCTTCCGGCTCTCGACCGTGGCAAGAAACGTCCTCGTTCAGGTCCTGA 3720
QY 3721 TCGACGAGGAAATCGTCTGCTGTTGCTGGCGACCACTACACGAAATTCATATGGGAGA 3780
Db 3721 TCGACGAGGAAATCGTCTGCTGTTGCTGGCGACCACTACACGAAATTCATATGGGAGA 3780
QY 3781 AGTACGCAAGCTGTGCCGACGGCGGACGAGATGTTTGCATATTTTCAGTCGCGACGGG 3840
Db 3781 AGTACGCAAGCTGTGCCGACGGCGGACGAGATGTTTGCATATTTTCAGTCGCGACGGG 3840
QY 3841 AGCGCTACCGCTCAAGCTGGAACCTTCGCGCTCATGTGCGGATCGGATTCACACCGCG 3900
Db 3841 AGCGCTACCGCTCAAGCTGGAACCTTCGCGCTCATGTGCGGATCGGATTCACACCGCG 3900
QY 3901 TGAAGAAGTGGCGGACGAGTGGGGAAGCTCGGAAGCTTGCAGGAGCGGCGCTGG 3960
Db 3901 TGAAGAAGTGGCGGACGAGTGGGGAAGCTCGGAAGCTTGCAGGAGCGGCGCTGG 3960
QY 3961 TGGAACACGCTGGGTCAATGATGACCTGTGTGATTTGCAAAACGCTAGGCGCTTGTGGGT 4020
Db 3961 TGGAACACGCTGGGTCAATGATGACCTGTGTGATTTGCAAAACGCTAGGCGCTTGTGGGT 4020
QY 4021 CAGTTCGGCTGGGGTTACAGCAGCAGCGCTTTTACTGGCATTTCTAGTTGACGCTTT 4080
Db 4021 CAGTTCGGCTGGGGTTACAGCAGCAGCGCTTTTACTGGCATTTCTAGTTGACGCTTT 4080
QY 4081 CTGATGGGCTGCCTGTATCGAGTGGTGATTTTGTGCCGAGCTGCCGTCGGGAGCTGTT 4140
Db 4081 CTGATGGGCTGCCTGTATCGAGTGGTGATTTTGTGCCGAGCTGCCGTCGGGAGCTGTT 4140
QY 4141 GGCTGGCTGGGAGATATATGTTGGTGTAAACAAATGACGCTTAGCATTTCTAGTTGACGCTTT 4200
Db 4141 GGCTGGCTGGGAGATATATGTTGGTGTAAACAAATGACGCTTAGCATTTCTAGTTGACGCTTT 4200
QY 4201 ACACATTCGGGAGCTTTTAAATGATCTAGTGGGCTATCCCCGGGGGATATCCATAGGCCCG 4260
Db 4201 ACACATTCGGGAGCTTTTAAATGATCTAGTGGGCTATCCCCGGGGGATATCCATAGGCCCG 4260
QY 4261 ATCTAGTAACATAATGACACCGCGCGATAATTTTATCTAGTTTGGCGCTATATTTTG 4320
Db 4261 ATCTAGTAACATAATGACACCGCGCGATAATTTTATCTAGTTTGGCGCTATATTTTG 4320
QY 4321 TTTTCTATCGGCTATTAATGATATATGTTGGGACTCTAATCATATAAAACCCATCTCAT 4380
Db 4321 TTTTCTATCGGCTATTAATGATATATGTTGGGACTCTAATCATATAAAACCCATCTCAT 4380
QY 4381 AATAAGCTCATGATTCATGTTTAAATTTATTTACATGCTTAACGTTAATTCACAGAAATAT 4440
Db 4381 AATAAGCTCATGATTCATGTTTAAATTTATTTACATGCTTAACGTTAATTCACAGAAATAT 4440
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QY 4441 ATGATAATCATCGCAAGACCGCAACAGGATTCATCTTAAGAACTTTATTCGCAATG 4500
Db 4441 ATGATAATCATCGCAAGACCGCAACAGGATTCATCTTAAGAACTTTATTCGCAATG 4500
QY 4501 TTTGAACGATCGTTCGTCGAGCTATGGGCCGA 4533
Db 4501 TTTGAACGATCGTTCGTCGAGCTATGGGCCGA 4533

RESULT 7
US-09-845-064-6
; Sequence 6, Application US/09845064
; Publication No. US20030175976A1
; GENERAL INFORMATION:
; APPLICANT: MERISTEM THERAPEUTICS
; TITLE OF INVENTION: CLEAN SYNTHETIC VECTORS, PLASMIDS, TRANSGENIC PLANTS
; TITLE OF INVENTION: AND PLANT PARTS CONTAINING SAID VECTORS, AND THEIR
; TITLE OF INVENTION: METHODS OF PRODUCTION
; FILE REFERENCE: SynVec1
; CURRENT APPLICATION NUMBER: US/09/845,064
; CURRENT FILING DATE: 2001-04-27
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 6016
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Plasmid
; OTHER INFORMATION: pmr1122
; FEATURE:
; NAME/KEY: rep_origin
; LOCATION: (1)..(654)
; OTHER INFORMATION: Origin of replication ori RK2
; FEATURE:
; NAME/KEY: rep_origin
; LOCATION: (655)..(1263)
; OTHER INFORMATION: Origin of replication ori Cole1
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1264)..(2603)
; OTHER INFORMATION: NPT III gene coding for neomycin
; OTHER INFORMATION: phosphotransferase and kanamycin resistance
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (2604)..(4098)
; OTHER INFORMATION: TrfA locus coding for two proteins, p285 and p382,
; OTHER INFORMATION: enabling the increase in the rate of replication
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (4105)..(4271)
; OTHER INFORMATION: T-DNA left border
; FEATURE:
; NAME/KEY: terminator
; LOCATION: (4272)..(4559)
; OTHER INFORMATION: No. US20030175976Alaline synthetase terminator
; FEATURE:
; NAME/KEY: gene
; LOCATION: (4560)..(5556)
; OTHER INFORMATION: Wild type NPT II gene coding for neomycin
; OTHER INFORMATION: phosphotransferase and kanamycin resistance
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (5557)..(5770)
; OTHER INFORMATION: No. US20030175976Alaline synthetase promoter
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (5770)..(5836)
; OTHER INFORMATION: MCS multiple cloning site
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (5836)..(6009)
; OTHER INFORMATION: T-DNA right border
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US-09-845-064-6

Query Match	94.3%;	Score 4531.4;	DB 10;	Length 6016;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 4532;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
Qy	1	CCGGGCTGGTTCGCTCGCTCGCTGGGCTGGCGGCGGTCTATGGCCCTGCAAAAGCGCCGAG	60	
Db	1	CCGGGCTGGTTCGCTCGCTCGCTGGGCTGGCGGCGGTCTATGGCCCTGCAAAAGCGCCGAG	60	
Qy	61	AAACGCGCGTGGAGCCGTGTGCGAGACAACCGCGGCCCGCGGCTGTGTGGATACCTCGCGG	120	
Db	61	AAACGCGCGTGGAGCCGTGTGCGAGACAACCGCGGCCCGCGGCTGTGTGGATACCTCGCGG	120	
Qy	121	AAAACTTGGCCCTCAGTCAGAGATGAGGGGGGAGCTTGACACTTGAAGGGGCGCACTCAC	180	
Db	121	AAAACTTGGCCCTCAGTCAGAGATGAGGGGGGAGCTTGACACTTGAAGGGGCGCACTCAC	180	
Qy	181	CCGGCGCGGCGTGTGACAGATGAGGGGCGAGGCTCGATTTCGGCCGGCGACGTGAGCTGGC	240	
Db	181	CCGGCGCGGCGTGTGACAGATGAGGGGCGAGGCTCGATTTCGGCCGGCGACGTGAGCTGGC	240	
Qy	241	CAGCCTCGCAAAATCGGCGAAACCGCTGATTTTACGGGAGTTTCCCAACAGATATGTGGA	300	
Db	241	CAGCCTCGCAAAATCGGCGAAACCGCTGATTTTACGGGAGTTTCCCAACAGATATGTGGA	300	
Qy	301	CAAGCCTGGGGATAAGTGCCTCGGCTATTGACACTTTGAGGGGCGCACTACTGACAGAT	360	
Db	301	CAAGCCTGGGGATAAGTGCCTCGGCTATTGACACTTTGAGGGGCGCACTACTGACAGAT	360	
Qy	361	GAGGGGCGGATCCTTGACACTTGAGGGGCGAGTGTGACAGATGAGGGGCGCACTAT	420	
Db	361	GAGGGGCGGATCCTTGACACTTGAGGGGCGAGTGTGACAGATGAGGGGCGCACTAT	420	
Qy	421	TGACATTTGAGGGGCTGTCCACAGGCGAGAAATCCAGCATTTGCAAGGGTTTCGCGCCGT	480	
Db	421	TGACATTTGAGGGGCTGTCCACAGGCGAGAAATCCAGCATTTGCAAGGGTTTCGCGCCGT	480	
Qy	481	TTTTTCGGCCACCGCTAACCTGTCTTTTAAACCTGCTTTTAAACCAATATTTATAACCTTG	540	
Db	481	TTTTTCGGCCACCGCTAACCTGTCTTTTAAACCTGCTTTTAAACCAATATTTATAACCTTG	540	
Qy	541	TTTTTAAACAGGGCTGCGCCCTGTGCGGCTGACCGCGCACCGCAAGGGGGGTGCCCCC	600	
Db	541	TTTTTAAACAGGGCTGCGCCCTGTGCGGCTGACCGCGCACCGCAAGGGGGGTGCCCCC	600	
Qy	601	CTTCTCGAAACCTCCCGAAAGGTATGCGGTGTGAAATACCGCACAGATGCGTAAGGAGA	660	
Db	601	CTTCTCGAAACCTCCCGAAAGGTATGCGGTGTGAAATACCGCACAGATGCGTAAGGAGA	660	
Qy	661	AAATAACGCAATCAGCGGCTCTTCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTGCTT	720	
Db	661	AAATAACGCAATCAGCGGCTCTTCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTGCTT	720	
Qy	721	CGGCTGCGGCGAGCGGTATCAGCTCACTCAAGAGCGGTATACGGTTATCCACAGAAATCA	780	
Db	721	CGGCTGCGGCGAGCGGTATCAGCTCACTCAAGAGCGGTATACGGTTATCCACAGAAATCA	780	
Qy	781	GGGGATAACCGAGGAAAGAAACATGTGACAAAGGCCAGCAAAAGGCCAGGAAACCGTAAA	840	
Db	781	GGGGATAACCGAGGAAAGAAACATGTGACAAAGGCCAGCAAAAGGCCAGGAAACCGTAAA	840	
Qy	841	AAGCGCGGTTGCTGGGCTTTTTCATAGGCTCGGCCCGCTGACGAGCATCAAAAAT	900	
Db	841	AAGCGCGGTTGCTGGGCTTTTTCATAGGCTCGGCCCGCTGACGAGCATCAAAAAT	900	
Qy	901	CGAGCTCAAGTCAGAGGTGCGGAAACCCGACAGGACTATAAGAGTACCAGGCGTTTCCC	960	
Db	901	CGAGCTCAAGTCAGAGGTGCGGAAACCCGACAGGACTATAAGAGTACCAGGCGTTTCCC	960	
Qy	961	CCTCGAAGCTCCCTCGTGCCTCTCTGTTCCGACCTGCGCTTACCGGATACCTGTCC	1020	
Db	961	CCTCGAAGCTCCCTCGTGCCTCTCTGTTCCGACCTGCGCTTACCGGATACCTGTCC	1020	

Qy	2101	CGAGCTGTATCGCGAGTGCATCAGGCTCTTTCACCTCCATCGACATATCGGATTCCTTA	2160
Db	2101	CGAGCTGTATCGCGAGTGCATCAGGCTCTTTCACCTCCATCGACATATCGGATTCCTTA	2160
Qy	2161	TACCAATAGCTTACACAGCCGCTTAGCCGAATTCGATTTACTTACTGAATACGATCTGGC	2220
Db	2161	TACCAATAGCTTACACAGCCGCTTAGCCGAATTCGATTTACTTACTGAATACGATCTGGC	2220
Qy	2221	CGATGTGGATTCGAAATCGGGAAGAGACACTCCATTTAAAGATCCGGCCGAGCTGTA	2280
Db	2221	CGATGTGGATTCGGAATCGGGAAGAGACACTCCATTTAAAGATCCGGCCGAGCTGTA	2280
Qy	2281	TGATTTTAAAGACGGAAGCCCGAAGAGAACTTGTCTTTTCCACGCGACCTGGG	2340
Db	2281	TGATTTTAAAGACGGAAGCCCGAAGAGAACTTGTCTTTTCCACGCGACCTGGG	2340
Qy	2341	AGACAGCAACATCTTCTGGAAGATGCCAAGTAAGTGGCTTTATTGATCTTGGGAGAAG	2400
Db	2341	AGA CAGCAACATCTTCTGGAAGATGGCAAAGTAAGTGGCTTTATTGATCTTGGGAGAAG	2400
Qy	2401	CGGAGGCGGACAAAGTGGTATGACATTTGCTTCTCGGTCCGGTCCGATCAGGGAGGATAT	2460
Db	2401	CGGAGGCGGACAAAGTGGTATGACATTTGCTTCTCGGTCCGGTCCGATCAGGGAGGATAT	2460
Qy	2461	CGGGGAAGAACAGTATGTGAGCTATTTTGTACTTACTGGGATCAAGCCTGATTGGGA	2520
Db	2461	CGGGGAAGAACAGTATGTGAGCTATTTTGTACTTACTGGGATCAAGCCTGATTGGGA	2520
Qy	2521	GAATAATAATATTTACTTGGATGAATTTGTTTAGTACCTAGATGTGGCGCAACG	2580
Db	2521	GAATAATAATATTTACTTGGATGAATTTGTTTAGTACCTAGATGTGGCGCAACG	2580
Qy	2581	ATGCCGCGCAAGCAGGAGCGCACCTTCTTCTCGCATCAAGTGTGTTTGGCTCTCAGG	2640
Db	2581	ATGCCGCGCAAGCAGGAGCGCACCTTCTTCTCGCATCAAGTGTGTTTGGCTCTCAGG	2640
Qy	2641	CCGAGGCCCAAGCAAGTATTTGGGCAAGGGTCCGCTGGTATTCGTGCAGGGCAAGATTC	2700
Db	2641	CCGAGGCCCAAGCAAGTATTTGGGCAAGGGTCCGCTGGTATTCGTGCAGGGCAAGATTC	2700
Qy	2701	GGATACCAAGTACGAGAAGAGCGGCCAGACGGTCTACGGGACCGACTTCATTTGCCGATA	2760
Db	2701	GGATACCAAGTACGAGAAGAGCGGCCAGACGGTCTACGGGACCGACTTCATTTGCCGATA	2760
Qy	2761	AGGTGGATTTCTCGACACCAAGCACAGCGCGGTCAAATCAGGAATAAGGGCACATTG	2820
Db	2761	AGGTGGATTTCTCGACACCAAGCACAGCGCGGTCAAATCAGGAATAAGGGCACATTG	2820
Qy	2821	CCCGCGGTGAGTCGGGGCAATCCCGCAAGAGGGTGAATGAATCGGACGTTTTGACCGGA	2880
Db	2821	CCCGCGGTGAGTCGGGGCAATCCCGCAAGAGGGTGAATGAATCGGACGTTTTGACCGGA	2880
Qy	2881	AGGCATACAGCAAGAACTGATCGACCGGGGTTTTCCGGCCGAGGATGCGCAAAACCATCG	2940
Db	2881	AGGCATACAGCAAGAACTGATCGACCGGGGTTTTCCGGCCGAGGATGCGCAAAACCATCG	2940
Qy	2941	CAAGCCGACCGTCATCGCTGCGCCCGCGCAAACTTCCAGTCCGTCGGTTCGATGGTCC	3000
Db	2941	CAAGCCGACCGTCATCGCTGCGCCCGCGCAAACTTCCAGTCCGTCGGTTCGATGGTCC	3000
Qy	3001	AGCAAGCTACGGCCAAAGATCGAGCGCACGCTGCAACTGGCTTCCCTCGCTCGCCCG	3060
Db	3001	AGCAAGCTACGGCCAAAGATCGAGCGCGACAGCTGCAACTGGCTTCCCTCGCTCGCCCG	3060
Qy	3061	CGCCATCGGCCCGCTGGAGGTTTCGCTCTCGAAAGAGGCGGCAAGTTTGGCGA	3120
Db	3061	CGCCATCGGCCCGCTGGAGGTTTCGCTCTCGAAAGAGGCGGCAAGTTTGGCGA	3120
Qy	3121	AGTCGATGACCATCGACCGGAGGACTATGACGACAGAGCGGCAAAACCCCGCGCG	3180
Db	3121	AGTCGATGACCATCGACCGGAGGAACTATGACGACCAAGAGCGGCAAAACCCCGCGCG	3180
Qy	3181	AGGACCTGGCAAAACAGGTGAGGAGGCAAGAGGCGCGTGTCTGTAACACACGGAAGC	3240

Db	3181	AGGACCTGGCAAAACAGGTGAGGAGGCAAGAGGCGCGTGTCTGTAACACACGGAAGC	3240
Qy	3241	AGCAGATCAAGGAAATGCAGCTTTCTTGTTCGATATTGCGCGCGTGGCCGACACGATGC	3300
Db	3241	AGCAGATCAAGGAAATGCAGCTTTCTTGTTCGATATTGCGCGCGTGGCCGACACGATGC	3300
Qy	3301	GAGCGATGCCAAACGACACAGCGCCGCTCTGCGCTTTTCCACGCGCAACAAGAAAAATCC	3360
Db	3301	GAGCGATGCCAAACGACACAGCGCCGCTCTGCGCTTTTCCACGCGCAACAAGAAAAATCC	3360
Qy	3361	CGCGGAGGCGCTGCAAAACAAGGTCAATTTTCAACGTCACAAGGAGCTGAAGATCACCT	3420
Db	3361	CGCGGAGGCGCTGCAAAACAAGGTCAATTTTCCACGTCACAAGGAGCTGAAGATCACCT	3420
Qy	3421	ACACCGCGCTCGAGCTCGCGGCGAGATCAAGAACGAACTGGTGTGGCAGCAGGTGTTGAGT	3480
Db	3421	ACACCGCGCTCGAGCTCGCGGCGAGATCAAGAACGAACTGGTGTGGCAGCAGGTGTTGAGT	3480
Qy	3481	ACGCAAGCGCACCCCTTATCGGCGAGCCGATCACTTTTCACTGTTCTACGAGCTTTGCCAGG	3540
Db	3481	ACGCAAGCGCACCCCTTATCGGCGAGCCGATCACTTTTCACTGTTCTACGAGCTTTGCCAGG	3540
Qy	3541	ACCTGGGCTGGTTCGATCAATGCGCGGATTTTACACGAAGCCGAGGAATGCTGTGCGGCC	3600
Db	3541	ACCTGGGCTGGTTCGATCAATGCGCGGATTTTACACGAAGCCGAGGAATGCTGTGCGGCC	3600
Qy	3601	TACAGCGAGCGGATGGGCTTCACTGTCGACCGCTGGGCACTTGGCAATCGGTGTGCG	3660
Db	3601	TACAGCGAGCGGATGGGCTTCACTGTCGACCGCTGGGCACTTGGCAATCGGTGTGCG	3660
Qy	3661	TGCTGCAACCGCTTCCGCGTCTCGGACCGTGGCAAGAAACGTCCTGTTGCCAGGTCCTGA	3720
Db	3661	TGCTGCAACCGCTTCCGCGTCTCGGACCGTGGCAAGAAACGTCCTGTTGCCAGGTCCTGA	3720
Qy	3721	TCGACGAGGAAATCGTCTGCTGTTTGTCTGGGCACTACACGAAATTCATATGGGAGA	3780
Db	3721	TCGACGAGGAAATCGTCTGCTGTTTGTCTGGGCACTACACGAAATTCATATGGGAGA	3780
Qy	3781	AGTACCGCAAGCTGTCCCGACCGCGCGGATGTTTCGACTATTTTCAGCTCCGACCGGG	3840
Db	3781	AGTACCGCAAGCTGTCCCGACCGCGCGGATGTTTCGACTATTTTCAGCTCCGACCGGG	3840
Qy	3841	AGCGGTACCGCTCAAGCTGGAACCTTCCGCTCATGTGCGGATCGGATTCACACCGCG	3900
Db	3841	AGCGGTACCGCTCAAGCTGGAACCTTCCGCTCATGTGCGGATCGGATTCACACCGCG	3900
Qy	3901	TGAAGAAGTGGCGGAGCAGGTTCGGCAAGCTTCGCAAGAGTTGCGAGGCGAGCGGCTGG	3960
Db	3901	TGAAGAAGTGGCGGAGCAGGTTCGGCAAGCTTCGCAAGAGTTGCGAGGCGAGCGGCTGG	3960
Qy	3961	TGGAACAACGCTGGGTCAATGATGACCTGGTGCATTTGCAAAACCTAGGGCTTTGTGGGT	4020
Db	3961	TGGAACAACGCTGGGTCAATGATGACCTGGTGCATTTGCAAAACCTAGGGCTTTGTGGGT	4020
Qy	4021	CAGTTCGGCTGGGGTTTCAAGCAGCAGCGCTTTTACTGGCATTTTCTAGGTTCACGCTTT	4080
Db	4021	CAGTTCGGCTGGGGTTTCAAGCAGCAGCGCTTTTACTGGCATTTTCTAGGTTCACGCTTT	4080
Qy	4081	CTGATGGGCTGCTGATCGAGTGGTGAATTTGTGCGGAGCTCCGGTTCGGGAGCTGTT	4140
Db	4081	CTGATGGGCTGCTGATCGAGTGGTGAATTTGTGCGGAGCTCCGGTTCGGGAGCTGTT	4140
Qy	4141	GGCTGGCTGGCAGGATATATTGTTGTTGTAACAAATTCAGCGCTTAGACAACCTTAATA	4200
Db	4141	GGCTGGCTGGCAGGATATATTGTTGTTGTAACAAATTCAGCGCTTAGACAACCTTAATA	4200
Qy	4201	ACACATTCGGGAGCTTTTAAATGCTAGTGGGCTATCCCGGGGGATATCCATAGGCCCG	4260
Db	4201	ACACATTCGGGAGCTTTTAAATGCTAGTGGGCTATCCCGGGGGATATCCATAGGCCCG	4260
Qy	4261	ATCTAGTAACATAATGACACCGCGCGGATTAATTTTATCTCTAGTTTTCGCGCTATTTTG	4320

Db 4261 ATCTAGTAACATAATGACACCGCGCGGATAATTATTCCTAGTTTGGCGCTATATTTTG 4320  
Qy 4321 TTTTCTATCGGTAATTAATGTATAATTGGGGAGCTCTAATCATATAAAACCCATCTCATTA 4380  
Db 4321 TTTTCTATCGGTAATTAATGTATAATTGGGGAGCTCTAATCATATAAAACCCATCTCATTA 4380  
Qy 4381 AATAACGTCATGCATTAACATGTTAATTATTACATGCTTAAACGTAATTAACAGAAATTA 4440  
Db 4381 AATAACGTCATGCATTAACATGTTAATTATTACATGCTTAAACGTAATTAACAGAAATTA 4440  
Qy 4441 ATGATAATCATCGCAACCGCGCAACAGGATTCATCTTAAGAACTTTATGCAAAATG 4500  
Db 4441 ATGATAATCATCGCAACCGCGCAACAGGATTCATCTTAAGAACTTTATGCAAAATG 4500  
Qy 4501 TTTGAACGATCGTTGCTGCGAGCTAATGGCCCGA 4533  
Db 4501 TTTGAACGATCGTTGCTGCGAGCTAATGGCCCGA 4533

RESULT 8

US-09-845-064-5  
; Sequence 5, Application US/09845064  
; Publication No. US20030175976A1  
; GENERAL INFORMATION:  
; APPLICANT: MERISTEM THERAPEUTICS  
; TITLE OF INVENTION: CLEAN SYNTHETIC VECTORS, PLASMIDS, TRANSGENIC PLANTS  
; TITLE OF INVENTION: AND PLANT PARTS CONTAINING SAID VECTORS, AND THEIR  
; FILE REFERENCE: Synvec1  
; CURRENT APPLICATION NUMBER: US/09/845.064  
; CURRENT FILING DATE: 2001-04-27  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 6017  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE: Description of Artificial Sequence:Plasmid  
; OTHER INFORMATION: pmr1121  
; FEATURE:  
; NAME/KEY: rep origin  
; LOCATION: (1)-(654)  
; OTHER INFORMATION: Origin of replication ori RK2  
; FEATURE:  
; NAME/KEY: rep origin  
; LOCATION: (1264)..(2603)  
; OTHER INFORMATION: NPT III gene coding for neomycin  
; OTHER INFORMATION: phosphotransferase and kanamycin resistance  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (2604)..(4098)  
; OTHER INFORMATION: Trifa locus coding for two proteins, P285 and P382,  
; OTHER INFORMATION: enabling the increase in the rate of replication  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (4106)..(4271)  
; OTHER INFORMATION: T-DNA left border  
; FEATURE:  
; NAME/KEY: terminator  
; LOCATION: (4272)..(4559)  
; OTHER INFORMATION: No. US20030175976Ala1line synthetase terminator  
; FEATURE:  
; NAME/KEY: gene  
; LOCATION: (4560)..(5556)  
; OTHER INFORMATION: NPT II gene coding for neomycin phosphotransferase  
; OTHER INFORMATION: and kanamycin resistance  
; FEATURE:  
; NAME/KEY: misc\_difference

; LOCATION: (5559)  
; OTHER INFORMATION: BspEI restriction site introduced with respect to  
; OTHER INFORMATION: pmr1119  
; FEATURE:  
; NAME/KEY: promoter  
; LOCATION: (5557)..(5771)  
; OTHER INFORMATION: No. US20030175976Ala1line synthetase promoter  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (5771)..(5837)  
; OTHER INFORMATION: MCS multiple cloning site  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (5837)..(6010)  
; OTHER INFORMATION: T-DNA right border  
; US-09-845-064-5  
Query Match 94.3%; Score 4531.4; DB 10; Length 6017;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 4532; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 CCGGGCTGTTGCCCTTCGCCGCTGGCGCGCTCTATGGCCCTCTATGGCCCTGCAAAACGCGCCAG 60  
Db 1 CCGGGCTGTTGCCCTTCGCCGCTGGCGCGCTCTATGGCCCTCTATGGCCCTGCAAAACGCGCCAG 60  
Qy 61 AAACGCGCTCGAAGCCGTGTGCGAGACACCGCGCGCGCGCGCTTGTGGATACCTTCGCGG 120  
Db 61 AAACGCGCTCGAAGCCGTGTGCGAGACACCGCGCGCGCGCGCTTGTGGATACCTTCGCGG 120  
Qy 121 AAAAATTGGCCCTCACTGACAGATGAGGGCGGACGTTGACACTTGAGGGCGCGACTCAC 180  
Db 121 AAAAATTGGCCCTCACTGACAGATGAGGGCGGACGTTGACACTTGAGGGCGCGACTCAC 180  
Qy 181 CCGGCGCGGCTTGA CAGATGAGGGCGAGCTCGATTTTGGCGCGGACGTTGAGCTGGC 240  
Db 181 CCGGCGCGGCTTGA CAGATGAGGGCGAGCTCGATTTTGGCGCGGACGTTGAGCTGGC 240  
Qy 241 CAGCCTCGCAAAATCGGGAACCGCTGATTTTACCGAGTTTCCACACAGATGATGTGA 300  
Db 241 CAGCCTCGCAAAATCGGGAACCGCTGATTTTACCGAGTTTCCACACAGATGATGTGA 300  
Qy 301 CAAAGCCTGGGGATAAGTGGCCCTGCGGTATTGACACTTGAGGGCGCGACTTACTGACAGAT 360  
Db 301 CAAAGCCTGGGGATAAGTGGCCCTGCGGTATTGACACTTGAGGGCGCGACTTACTGACAGAT 360  
Qy 361 GAGGGCGCGATCCTTTGACACTTTGAGGGCGAGAGTCTGACAGATGAGGGCGCGACTTAT 420  
Db 361 GAGGGCGCGATCCTTTGACACTTTGAGGGCGAGAGTCTGACAGATGAGGGCGCGACTTAT 420  
Qy 421 TGACATTTGAGGGGCTGTCCACAGGCGAGAAATCCAGCATTTTCAAGGGTTTCCGCCCGT 480  
Db 421 TGACATTTGAGGGGCTGTCCACAGGCGAGAAATCCAGCATTTTCAAGGGTTTCCGCCCGT 480  
Qy 481 TTTTTCGGCCACCCCTAAACCTGTCTTTTAACTCTCTTTTAAACCAATATTTATAAACCTTG 540  
Db 481 TTTTTCGGCCACCCCTAAACCTGTCTTTTAACTCTCTTTTAAACCAATATTTATAAACCTTG 540  
Qy 541 TTTTAAACAGGGCTGCGCCCTGTGCGGTGACCGCGACCGCGAAGGGGGTGCCCCC 600  
Db 541 TTTTAAACAGGGCTGCGCCCTGTGCGGTGACCGCGACCGCGAAGGGGGTGCCCCC 600  
Qy 601 CTTTCTGAACCCCTCCCGGAAGGTATGCGGTGTGAAATACCGCACAGATCGGTAAAGAGA 660  
Db 601 CTTTCTGAACCCCTCCCGGAAGGTATGCGGTGTGAAATACCGCACAGATCGGTAAAGAGA 660  
Qy 661 AAATACCGCATCAGGGCGCTCTTCGGTCTCTCCCTCACTGACTCGCTCGCTCGGTCGTT 720  
Db 661 AAATACCGCATCAGGGCGCTCTTCGGTCTCTCCCTCACTGACTCGCTCGCTCGGTCGTT 720  
Qy 721 CGGCTCGGCGAGCGGTATCAGCTCACTCAAAGGGGGTAATACGGTTATCCACAGAAATCA 780  
Db 721 CGGCTCGGCGAGCGGTATCAGCTCACTCAAAGGGGGTAATACGGTTATCCACAGAAATCA 780

Qy	781	GGGATTAACGCAAGAAAGACATGTGAGCAAAAAGGCCAGCAAAAAGCCAGGAACCGTAAA	840
Db	781	GGGGATTAACGCAAGAAAGAAACATGTGAGCAAAAAGGCCAGCAAAAAGCCAGGAACCGTAAA	840
Qy	841	AAGSCCGGTTGCTGCGGTTTTTCCATAGGCTCGCCCCCTGACGAGCATCAAAAAAT	900
Db	841	AAGSCCGGTTGCTGCGGTTTTTCCATAGGCTCGCCCCCTGACGAGCATCAAAAAAT	900
Qy	901	CGACGCTCAAGTCAAGAGTGGCGAAACCCGACAGGACTATAAAGATACCAAGGCGTTTCCC	960
Db	901	CGACGCTCAAGTCAAGAGTGGCGAAACCCGACAGGACTATAAAGATACCAAGGCGTTTCCC	960
Qy	961	CTTGGAAGCTCCCTGCTGCGCTCTCTGTTCCGACCTCGCGCTTACCGGATACCTGTCC	1020
Db	961	CCTGGAAGCTCCCTGCTGCGCTCTCTGTTCCGACCTCGCGCTTACCGGATACCTGTCC	1020
Qy	1021	GCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGT	1080
Db	1021	GCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGT	1080
Qy	1081	TCGGTGTAGGTTCGCTCCAAAGCTGGGCTGTGTGCACGAACCCGCCGTTTCAGCCCGAC	1140
Db	1081	TCGGTGTAGGTTCGCTCCAAAGCTGGGCTGTGTGCACGAACCCGCCGTTTCAGCCCGAC	1140
Qy	1141	CGCTGCGCCTTATCCGGTAACTATCGCTTTGAGTCCAAACCCGGTAAAGACACGACTTATCG	1200
Db	1141	CGCTGCGCCTTATCCGGTAACTATCGCTTTGAGTCCAAACCCGGTAAAGACACGACTTATCG	1200
Qy	1201	CCACTGGCAGAGCCTTCTACCATTAATCCGCGATAAACCCAGCGAACCATTTGAGGTGAT	1260
Db	1201	CCACTGGCAGAGCCTTCTACCATTAATCCGCGATAAACCCAGCGAACCATTTGAGGTGAT	1260
Qy	1261	AGGTAAGATTATACCGAGGTATGAAAACGAGAAATGGACCTTTACAGAAATTTACTCTATGA	1320
Db	1261	AGGTAAGATTATACCGAGGTATGAAAACGAGAAATGGACCTTTACAGAAATTTACTCTATGA	1320
Qy	1321	AGCGCCCATATTTAAAAAGCTACCAAGACGAAGAGGATGAAGAGGATGAGGAGGCAGATTG	1380
Db	1321	AGCGCCCATATTTAAAAAGCTACCAAGACGAAGAGGATGAAGAGGATGAGGAGGCAGATTG	1380
Qy	1381	CCTTGAATATATTGCAATACTGATAAGATAAATACATCTTTTATATAGAAGATATCGCCG	1440
Db	1381	CCTTGAATATATTGCAATACTGATAAGATAAATACATCTTTTATATAGAAGATATCGCCG	1440
Qy	1441	TATGTAAAGATTTCAGGGGCAAGGCATAGSCAGCGCGCTTATCAATATATCTATAGAT	1500
Db	1441	TATGTAAAGATTTCAGGGGCAAGGCATAGSCAGCGCGCTTATCAATATATCTATAGAT	1500
Qy	1501	GGGCAAGCATAAAACTTCGATGGACTAATGCTTGAACCCAGGACAATAACCTTATAG	1560
Db	1501	GGGCAAGCATAAAACTTCGATGGACTAATGCTTGAACCCAGGACAATAACCTTATAG	1560
Qy	1561	CTTGTAAATTTCTACCAAAATTTGGTTTCAAAATTCGGCTCCGTCGATACATAGTTATACG	1620
Db	1561	CTTGTAAATTTCTACCAAAATTTGGTTTCAAAATTCGGCTCCGTCGATACATAGTTATACG	1620
Qy	1621	CCAACCTTTGAAAAACAATTTGAAAAAGCTGTTTTCTGGTATTAAAGTTTTTGAAGTGCAA	1680
Db	1621	CCAACCTTTGAAAAACAATTTGAAAAAGCTGTTTTCTGGTATTAAAGTTTTTGAAGTGCAA	1680
Qy	1681	GGAAACAGTGAATTTGGAGTTTCGCTTGTGTATAAATTTAGCTTCTTGGGGTATCTTTAAATACT	1740
Db	1681	GGAAACAGTGAATTTGGAGTTTCGCTTGTGTATAAATTTAGCTTCTTGGGGTATCTTTAAATACT	1740
Qy	1741	GTAGAAAAGAGGAAGGAATAAATAATGGCTAAAAATGAGAAATATCACCGGAATGAAAAA	1800
Db	1741	GTAGAAAAGAGGAAGGAATAAATAATGGCTAAAAATGAGAAATATCACCGGAATGAAAAA	1800
Qy	1801	ACTGATCGAAAAATACCGCTGCGTAAAGATACGGAAGGAATGCTCTCTGCTTAAGGTATA	1860
Db	1801	ACTGATCGAAAAATACCGCTGCGTAAAGATACGGAAGGAATGCTCTCTGCTTAAGGTATA	1860
Qy	1861	TAAGCTGGTGGGAGAAAAATGAAAAACCTATATTTAAAAATGACGGACAGCCGGTATAAAGG	1920

Db	1861	TAAGCTGGTGGGAGAAAAATGAAAAACCTATATTTAAAAATGACGGACAGCCGGTATAAAGG	1920
Qy	1921	GACCACTTATGATGTGGAAAGGAAAGGACATGATGCTATGCTGGAAGGAAGCTGCC	1980
Db	1921	GACCACTTATGATGTGGAAAGGAAAGGACATGATGCTATGCTGGAAGGAAGCTGCC	1980
Qy	1981	TGTTCCAAAGGTCCTGCACCTTTGAAAGGCAATGATGGCTGGAGCAATCTGCTCATGAGTGA	2040
Db	1981	TGTTCCAAAGGTCCTGCACCTTTGAAAGGCAATGATGGCTGGAGCAATCTGCTCATGAGTGA	2040
Qy	2041	GGCCGATGGGCTCCTTTGCTCGGAAGATGAAAGATGAACAAAGCCCTGAAAGATAT	2100
Db	2041	GGCCGATGGGCTCCTTTGCTCGGAAGATGAAAGATGAACAAAGCCCTGAAAGATAT	2100
Qy	2101	CGAGCTGTATGCGGAGTGCAATCAGGCTCTTTCACTCCATCGACATATCGGATTTGCCCTA	2160
Db	2101	CGAGCTGTATGCGGAGTGCAATCAGGCTCTTTCACTCCATCGACATATCGGATTTGCCCTA	2160
Qy	2161	TACGAATAGCTTAGACAGACCGCTTAGCCGAATTTGGATTTACTTACTGAATAACGATCTGGC	2220
Db	2161	TACGAATAGCTTAGACAGACCGCTTAGCCGAATTTGGATTTACTTACTGAATAACGATCTGGC	2220
Qy	2221	CGATGTGGATTTGCGAAACCTGGGAAAGACACTCCAATTTAAAGATCCCGCGAGCTGTA	2280
Db	2221	CGATGTGGATTTGCGAAACCTGGGAAAGACACTCCAATTTAAAGATCCCGCGAGCTGTA	2280
Qy	2281	TGATTTTTTAAAGACGGAAAGCCGAAAGAGAACTTGCTTTTCCACCGCGACCTGGG	2340
Db	2281	TGATTTTTTAAAGACGGAAAGCCGAAAGAGAACTTGCTTTTCCACCGCGACCTGGG	2340
Qy	2341	AGACAGCAACATCTTTGTGAAAGATGGCAAGTAAAGTGGCTTTATTTGATCTTGGGAGAAG	2400
Db	2341	AGACAGCAACATCTTTGTGAAAGATGGCAAGTAAAGTGGCTTTATTTGATCTTGGGAGAAG	2400
Qy	2401	CGCAGGGCGGACAAGTGGTATGACATTTGCTTCTCGCTCCGTCGATCAGGAGGATAT	2460
Db	2401	CGCAGGGCGGACAAGTGGTATGACATTTGCTTCTCGCTCCGTCGATCAGGAGGATAT	2460
Qy	2461	CGGGGAAGAACAGTATGTCAGCTATTTTTTGACTTTTACGCGGATCAAGCTGATTTGGGA	2520
Db	2461	CGGGGAAGAACAGTATGTCAGCTATTTTTTGACTTTTACGCGGATCAAGCTGATTTGGGA	2520
Qy	2521	GAAAAATAAATAATATATTTTACTGATGAATTTGTTTTAGTACTAGATGCTGCGCAACG	2580
Db	2521	GAAAAATAAATAATATATTTTACTGATGAATTTGTTTTAGTACTAGATGCTGCGCAACG	2580
Qy	2581	ATGCCGGCGACAAGCAGGCGCACCGACTTCTTCCGCATCAAGTGTTTTGGCTCTCAGG	2640
Db	2581	ATGCCGGCGACAAGCAGGCGCACCGACTTCTTCCGCATCAAGTGTTTTGGCTCTCAGG	2640
Qy	2641	CCGAGGCCCAAGCAAGTATTTGGGCAAGGGGTGCTGGTATTTCTGTCAGGGCAAGTTTC	2700
Db	2641	CCGAGGCCCAAGCAAGTATTTGGGCAAGGGGTGCTGGTATTTCTGTCAGGGCAAGTTTC	2700
Qy	2701	GGAATACCAAGTACGAAAGGACGGCCAGACGGTCTACGGGACCGACTTCAATTTGCCGATA	2760
Db	2701	GGAATACCAAGTACGAAAGGACGGCCAGACGGTCTACGGGACCGACTTCAATTTGCCGATA	2760
Qy	2761	AGGTGGAATTTCTGGACACCAAGGCAAGGGGTGCTGGTATTTCTGTCAGGGCAAGTTTC	2820
Db	2761	AGGTGGAATTTCTGGACACCAAGGCAAGGGGTGCTGGTATTTCTGTCAGGGCAAGTTTC	2820
Qy	2821	CCCGCGGTGAGTTCGGGGCAATCCCGCAAGGAGGGTGAATGAATCGGAGTTTTCACCGGA	2880
Db	2821	CCCGCGGTGAGTTCGGGGCAATCCCGCAAGGAGGGTGAATGAATCGGAGTTTTCACCGGA	2880
Qy	2881	AGGCAATACAGGCAAGAACTGATCGACGCGGGTTTTTCCCGCAGGATCCGGAACCATCG	2940
Db	2881	AGGCAATACAGGCAAGAACTGATCGACGCGGGTTTTTCCCGCAGGATCCGGAACCATCG	2940
Qy	2941	CAAGCGCACCGCTCATGCTGCGTGGCGCCCGCGAAACCTTCCAGTCCGCTCGGTCGATGGTCC	3000

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Db 2941 CAAGCGCACCGTCATCGGTGGCGCCCGCGAAACCTTCCAGTCCGTCGGCTCGATGGTCC 3000
Qy 3001 AGCAAGCTACGGCCAGATCGAGCGCGACAGCGTGCAACTGGCTCCCTTCCCTGCGCTGCCG 3060
Db 3001 AGCAAGCTACGGCCAGATCGAGCGCGACAGCGTGCAACTGGCTCCCTTCCCTGCGCTGCCG 3060
Qy 3061 CGCATCGCGCGCGGTGGAGCGTTTCGGTCTCGTTCGAAACAGGAGCGCGAGGTTTGGCGA 3120
Db 3061 CGCATCGCGCGCGGTGGAGCGTTTCGGTCTCGTTCGAAACAGGAGCGCGAGGTTTGGCGA 3120
Qy 3121 AGTCGATGACCATCGACACGCGAGGAACTATGACGACCAAGAGCGGAAACCGCGCGCG 3180
Db 3121 AGTCGATGACCATCGACACGCGAGGAACTATGACGACCAAGAGCGGAAACCGCGCGCG 3180
Qy 3181 AGGACCTGGCAAAACAGGTGAGCGAGCGCAAGCAGGCGCGGTTCCTGAAACACACGAGC 3240
Db 3181 AGGACCTGGCAAAACAGGTGAGCGAGCGCAAGCAGGCGCGGTTCCTGAAACACACGAGC 3240
Qy 3241 AGCAGATCAAGGAAATCAGCTTTCCTTGTTCGATATTGGCGGTGGCGCGGACACGATGC 3300
Db 3241 AGCAGATCAAGGAAATCAGCTTTCCTTGTTCGATATTGGCGGTGGCGCGGACACGATGC 3300
Qy 3301 GAGCGATGCCAAACGACACGCGCGCGCTCGCCCTGTTTCCACGCGCGCAACAGAAATCC 3360
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Qy 3481 ACGGAAACGCGACCCCTATCGCGAGCGCGATCACTTTCAGCTTACGAGCTTTCGCCAGG 3540
Db 3481 ACGGAAACGCGACCCCTATCGCGAGCGCGATCACTTTCAGCTTACGAGCTTTCGCCAGG 3540
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Db 3541 ACTTGGCGTGTGATCAATGGCGCGGTATTACAGAAAGCGCGAGGAATGCTGTGGCGCC 3600
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Db 3661 TGCTGCAACCGCTTCCGCGCTCTCGACCGTGGCAAGAAACGTCGCGTTCGCGTCTCTGA 3720
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Qy 3781 AGTACCCCAAGCTCTCGCGAGCGCGCGAGGATTCGACTATTTCAGCTCGCACCGGG 3840
Db 3781 AGTACCCCAAGCTCTCGCGAGCGCGCGAGGATTCGACTATTTCAGCTCGCACCGGG 3840
Qy 3841 AGCCGTACCCGCTCAAGCTGGAACCTTCCGCTCATGTGCGGATCGGAATTCACCGCGG 3900
Db 3841 AGCCGTACCCGCTCAAGCTGGAACCTTCCGCTCATGTGCGGATCGGAATTCACCGCGG 3900
Qy 3901 TGAAGAAAGTGCGCGAGCAGGTGCGGCAAGCCTCGGAAGAGTTGCGAGGCGAGCGGCTGG 3960
Db 3901 TGAAGAAAGTGCGCGAGCAGGTGCGGCAAGCCTCGGAAGAGTTGCGAGGCGAGCGGCTGG 3960
Qy 3961 TGGAAACGCGCTGGTCAATGATGACCTGGTGCATTGCAACGCTAGGCGCTTGGGGT 4020
Db 3961 TGGAAACGCGCTGGTCAATGATGACCTGGTGCATTGCAACGCTAGGCGCTTGGGGT 4020
Qy 4021 CAGTTCCGGCTGGGGGTTTACGAGCGAGCGCTTACTGGCATTTCTAGGTTGACGCTT 4080
Db 4021 CAGTTCCGGCTGGGGGTTTACGAGCGAGCGCTTACTGGCATTTCTAGGTTGACGCTT 4080
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Qy 4081 CTGATGGCTGCTGTATCGAGTGTGATTTTGTGCGAGCTGCCGGTCCGGAGCTGTT 4140
Db 4081 CTGATGGCTGCTGTATCGAGTGTGATTTTGTGCGAGCTGCCGGTCCGGAGCTGTT 4140
Qy 4141 GGCTGGCTGGTGGCAGGATATATTGGTGTAAACAAATTTAGCGCTTAGACAACTTAATA 4200
Db 4141 GGCTGGCTGGTGGCAGGATATATTGGTGTAAACAAATTTAGCGCTTAGACAACTTAATA 4200
Qy 4201 ACACATTTGGGAGCTTTTAAATGTAATGCTGGGCTATCCCGGGGATATCCATAGGCCG 4260
Db 4201 ACACATTTGGGAGCTTTTAAATGTAATGTAATGCTGGGCTATCCCGGGGATATCCATAGGCCG 4260
Qy 4261 ATCTAGTAAACATAATGACACCGCGCGGATAATTTATCTAGTTTGGCGCTATATTTG 4320
Db 4261 ATCTAGTAAACATAATGACACCGCGCGGATAATTTATCTAGTTTGGCGCTATATTTG 4320
Qy 4321 TTTTCTATCGCTATTAAATGTATAATTTGGGACTCTAATATAAAACCCATCTCAT 4380
Db 4321 TTTTCTATCGCTATTAAATGTATAATTTGGGACTCTAATATAAAACCCATCTCAT 4380
Qy 4381 AATAAGCTCATGCAATTACATGTTAATTTATATACATGCTTAACGTAATTCACAGAAATTAT 4440
Db 4381 AATAAGCTCATGCAATTACATGTTAATTTATATACATGCTTAACGTAATTCACAGAAATTAT 4440
Qy 4441 ATGATAATCATCGCAAGCGCAACAGGATTCAATCTTAAAGAACTTTATTGCAAAATG 4500
Db 4441 ATGATAATCATCGCAAGCGCAACAGGATTCAATCTTAAAGAACTTTATTGCAAAATG 4500
Qy 4501 TTTGAACGATCGTTTCGTCGAGCTATGGGCCGA 4533
Db 4501 TTTGAACGATCGTTTCGTCGAGCTATGGGCCGA 4533
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## RESULT 9

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US-09-845-064-7
; Sequence 7, Application US/09845064
; Publication No. US20030175976A1
; GENERAL INFORMATION:
; APPLICANT: MERISTEM THERAPEUTICS
; TITLE OF INVENTION: CLEAN SYNTHETIC VECTORS, PLASMIDS, TRANSGENIC PLANTS
; TITLE OF INVENTION: AND PLANT PARTS CONTAINING SAID VECTORS, AND THEIR
; TITLE OF INVENTION: METHODS OF PRODUCTION
; FILE REFERENCE: SynVec1
; CURRENT APPLICATION NUMBER: US/09/845,064
; CURRENT FILING DATE: 2001-04-27
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 6017
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Plasmid
; OTHER INFORMATION: pMRT1155
; FEATURE:
; NAME/KEY: rep_origin
; LOCATION: (1)..(1654)
; OTHER INFORMATION: Origin of replication ori RK2
; FEATURE:
; NAME/KEY: rep_origin
; LOCATION: (655)..(1263)
; OTHER INFORMATION: Origin of replication ori ColEI
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1264)..(2603)
; OTHER INFORMATION: NPT III gene coding for neomycin
; OTHER INFORMATION: phosphotransferase and kanamycin resistance
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2604)..(4098)
; OTHER INFORMATION: TrfA locus coding for two proteins, P285 and P382,
; OTHER INFORMATION: enabling the increase in the rate of replication
```



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; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4106)..(4271)
; OTHER INFORMATION: T-DNA left border
; FEATURE:
; NAME/KEY: terminator
; LOCATION: (4272)..(4559)
; OTHER INFORMATION: No. US20030175976Alaline synthetase terminator
; FEATURE:
; NAME/KEY: gene
; LOCATION: (4560)..(5556)
; OTHER INFORMATION: Wild type NPT II gene coding for neomycin
; OTHER INFORMATION: transferase and kanamycin resistance
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (5557)..(5771)
; OTHER INFORMATION: No. US20030175976Alaline synthetase promoter
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (5771)..(5837)
; OTHER INFORMATION: MCS multiple cloning site
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (5837)..(6010)
; OTHER INFORMATION: T-DNA right border
US-09-845-064-7

Query Match      94.3%; Score 4531.4; DB 10; Length 6017;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4532; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCGGGCTGGTGGCCCTCCGCTGGGCTGGGCGGCGCTATGGCCCTGCAAGCGCGCAG 60
Db 1 CCGGGCTGGTGGCCCTCCGCTGGGCTGGGCGGCGCTATGGCCCTGCAAGCGCGCAG 60

Qy 61 AAACGCCGTGGAAGCGTGTGCGAGACACCGCGCGCCCGCGGTGTGGATACCTCGCG 120
Db 61 AAACGCCGTGGAAGCGTGTGCGAGACACCGCGCGCCCGCGGTGTGGATACCTCGCG 120

Qy 121 AAAACTGGCCCTCACTGACAGATGAGGGCGGACGTTGACACTTGAGGGCGGACTCAC 180
Db 121 AAAACTGGCCCTCACTGACAGATGAGGGCGGACGTTGACACTTGAGGGCGGACTCAC 180

Qy 181 CCGCGCGGGCGTTGACAGATGAGGGCGGACGCTCGATTTCGGCGCGGACGCTGGAGCTGGC 240
Db 181 CCGCGCGGGCGTTGACAGATGAGGGCGGACGCTCGATTTCGGCGCGGACGCTGGAGCTGGC 240

Qy 241 CAGCCTCGCAAAATCGGCGAAACCGCTGATTTTACGCGAGTTTCCCAAGATGATGGGA 300
Db 241 CAGCCTCGCAAAATCGGCGAAACCGCTGATTTTACGCGAGTTTCCCAAGATGATGGGA 300

Qy 301 CAGCCTGGGGATAAGTGCCTCGGTTATGACACTTGAGGGGGCGGACTACTGACAGAT 360
Db 301 CAGCCTGGGGATAAGTGCCTCGGTTATGACACTTGAGGGGGCGGACTACTGACAGAT 360

Qy 361 GAGGGGCGGATCCTTGACACTTGAGGGCGAGAGTGTGACAGATGAGGGGGCGGACCTAT 420
Db 361 GAGGGGCGGATCCTTGACACTTGAGGGCGAGAGTGTGACAGATGAGGGGGCGGACCTAT 420

Qy 421 TGACATTTGAGGGGCTGTCCACAGGCAAGAAATCCAGCAATTTGCAAGGGTTTCGCGCGGT 480
Db 421 TGACATTTGAGGGGCTGTCCACAGGCAAGAAATCCAGCAATTTGCAAGGGTTTCGCGCGGT 480

Qy 481 TTTTGGCCACCGCTAACCTGTCTTTTAACTGTTTAAACCAATTTTATAAACCCTTG 540
Db 481 TTTTGGCCACCGCTAACCTGTCTTTTAACTGTTTAAACCAATTTTATAAACCCTTG 540

Qy 541 TTTTAAACCGGCTGCGCCCTGTGCGCGTACCGCGACGCGAGGGGGTGCCTCC 600
Db 541 TTTTAAACCGGCTGCGCCCTGTGCGCGTACCGCGACGCGAGGGGGTGCCTCC 600

Qy 601 CTTCTCGAAACCTCCCGAAAGGTATGCGGTGTGAAATACCGCACAGATCGTAAGAGA 660
Db 601 CTTCTCGAAACCTCCCGAAAGGTATGCGGTGTGAAATACCGCACAGATCGTAAGAGA 660
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Db 601 CTTCTCGAAACCTCCCGAAAGGTATGCGGTGTGAAATACCGCACAGATCGTAAGAGA 660
Qy 661 AAATACCGCATCAGGCGCTCTCCGCTTCTCGCTCACTCACTCGCTCGCTCGCTCGT 720
Db 661 AAATACCGCATCAGGCGCTCTCCGCTTCTCGCTCACTCACTCGCTCGCTCGCTCGT 720
Qy 721 CGGCTCGGCGAGCGGTATCAGCTCACTCAAGCGCGTAAATACGGTTATCCACAGATCA 780
Db 721 CGGCTCGGCGAGCGGTATCAGCTCACTCAAGCGCGTAAATACGGTTATCCACAGATCA 780
Qy 781 GGGGATAACCGCAGAAAGACATGTGAGCAAAAGGCGCAGAAAGGCGCAGAAACCGTAAA 840
Db 781 GGGGATAACCGCAGAAAGACATGTGAGCAAAAGGCGCAGAAAGGCGCAGAAACCGTAAA 840
Qy 841 AAGGCGCGCTTGTGCGGTTTTTCCATAGGCTCGGCCCCCTGACGAGCATCACAAAAT 900
Db 841 AAGGCGCGCTTGTGCGGTTTTTCCATAGGCTCGGCCCCCTGACGAGCATCACAAAAT 900
Qy 901 CGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAAGGCTTCCC 960
Db 901 CGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAAGGCTTCCC 960
Qy 961 CTTGGAAGCTCCCTCGTGGCTCTCTGTTCCGACCTGCGCTTACCGGATACCTGTCC 1020
Db 961 CTTGGAAGCTCCCTCGTGGCTCTCTGTTCCGACCTGCGCTTACCGGATACCTGTCC 1020
Qy 1021 GCCTTTCTCCCTTCGGGAAGCGTGGCGCTTCTCATAGCTCAGCTGTAGGTATCTCAGT 1080
Db 1021 GCCTTTCTCCCTTCGGGAAGCGTGGCGCTTCTCATAGCTCAGCTGTAGGTATCTCAGT 1080
Qy 1081 TCGGTGTAGTTCGTTCCGCTCAAGCTGGGTGTGTCAGCAACCCCGCTTCAGCCGAC 1140
Db 1081 TCGGTGTAGTTCGTTCCGCTCAAGCTGGGTGTGTCAGCAACCCCGCTTCAGCCGAC 1140
Qy 1141 CGCTGGCGCTTATCCGCTAACTATCGTCTTGAAGTCCAAACCGGTGAAGACAGCTTATCG 1200
Db 1141 CGCTGGCGCTTATCCGCTAACTATCGTCTTGAAGTCCAAACCGGTGAAGACAGCTTATCG 1200
Qy 1201 CCACTGGCAGCGCTTCTACCAATAATCCGCGATAAACCCAGCGAACCATTTGAGGTGAT 1260
Db 1201 CCACTGGCAGCGCTTCTACCAATAATCCGCGATAAACCCAGCGAACCATTTGAGGTGAT 1260
Qy 1261 AGTAAAGATTTATACCGAGGTATGAAACCGAGAAATGGACCTTTACAGAAATTTACTCTATGA 1320
Db 1261 AGTAAAGATTTATACCGAGGTATGAAACCGAGAAATGGACCTTTACAGAAATTTACTCTATGA 1320
Qy 1321 AGCGCATATTTAAAAGCTACCAAGAGAGGATGAAGAGGATGAGAGGCGAGATTG 1380
Db 1321 AGCGCATATTTAAAAGCTACCAAGAGAGGATGAAGAGGATGAGAGGCGAGATTG 1380
Qy 1381 CTTTGAATATTTGACAATCTGATAGATAATACATCTTTTATATAGAGATATCGCCG 1440
Db 1381 CTTTGAATATTTGACAATCTGATAGATAATACATCTTTTATATAGAGATATCGCCG 1440
Qy 1441 TATGTAAAGATTTTACGGGGCAAGGATAGGCGCGCTTATCAATATATCTATAGAAT 1500
Db 1441 TATGTAAAGATTTTACGGGGCAAGGATAGGCGCGCTTATCAATATATCTATAGAAT 1500
Qy 1501 GGGCAAGCATAAAACTTGCATGGAATATGCTTGAACCCAGGACAATAACCTTATAG 1560
Db 1501 GGGCAAGCATAAAACTTGCATGGAATATGCTTGAACCCAGGACAATAACCTTATAG 1560
Qy 1561 CTTTGAATTTCTACCAAAATTTGGTTTCAAAATCGGCTCGCTTACCTATGTTATACG 1620
Db 1561 CTTTGAATTTCTACCAAAATTTGGTTTCAAAATCGGCTCGCTTACCTATGTTATACG 1620
Qy 1621 CCAACTTTGAAAAACAATTTGAAAAAGCTGTTTTCTGGTATTTAAGTTTTAGAAATGCAA 1680
Db 1621 CCAACTTTGAAAAACAATTTGAAAAAGCTGTTTTCTGGTATTTAAGTTTTAGAAATGCAA 1680
Qy 1681 GGAAACAGTGAATGGAGTTCGTTCTGTTATAAATAGCTTCTTGGGTATCTTTAAATACT 1740
Db 1681 GGAAACAGTGAATGGAGTTCGTTCTGTTATAAATAGCTTCTTGGGTATCTTTAAATACT 1740
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Qy	1741	GTAGAAAGAGGAGGAAATAATAATGGCTTAAATCGAGAAATATCACCGGAATTGAAAAA	1800
Db	1741	GTAGAAAGAGGAGGAAATAATAATGGCTTAAATCGAGAAATATCACCGGAATTGAAAAA	1800
Qy	1801	ACTGATCGAAAAATACCGCTGCGGTAAAGATACGGAAGGAATGTCTCTGCTAAGGTATA	1860
Db	1801	ACTGATCGAAAAATACCGCTGCGGTAAAGATACGGAAGGAATGTCTCTGCTAAGGTATA	1860
Qy	1861	TAAGCTGGTGGGAGAAAAAGAAACCTATATTTAAATAAGCAGGACAGCCGGTATAAAGG	1920
Db	1861	TAAGCTGGTGGGAGAAAAAGAAACCTATATTTAAATAAGCAGGACAGCCGGTATAAAGG	1920
Qy	1921	GACCACCTATGATGTGAAACGGGAAAGGACATGCTATGCTGGAAGGAAAGCTGCC	1980
Db	1921	GACCACCTATGATGTGAAACGGGAAAGGACATGCTATGCTGGAAGGAAAGCTGCC	1980
Qy	1981	TGTTCCAAAGGTCCTGCACCTTTGAACCGCATGATGGCTGGAGCAATCTGCTCATGAGTGA	2040
Db	1981	TGTTCCAAAGGTCCTGCACCTTTGAACCGCATGATGGCTGGAGCAATCTGCTCATGAGTGA	2040
Qy	2041	GGCGGATGGCGTCTTTGGCTCGGAAGAGTATGAAGATGAACAAAGCCCTGAAAAGATTAT	2100
Db	2041	GGCGGATGGCGTCTTTGGCTCGGAAGAGTATGAAGATGAACAAAGCCCTGAAAAGATTAT	2100
Qy	2101	CGAGCTGATGCGGAGTGCATCAGGCTCTTTCACTCCATCGACATATCGGATTTGCCCTA	2160
Db	2101	CGAGCTGATGCGGAGTGCATCAGGCTCTTTCACTCCATCGACATATCGGATTTGCCCTA	2160
Qy	2161	TACGAATAGCTTAGACAGCGCTTAGCCGAATTGGATTTACTTGAATAACGATCTGGC	2220
Db	2161	TACGAATAGCTTAGACAGCGCTTAGCCGAATTGGATTTACTTGAATAACGATCTGGC	2220
Qy	2221	CGATGTGGATTTGCAAACTGGGAAGAGACATCTCCATTTAAAGATCCGCGCAGCTGTA	2280
Db	2221	CGATGTGGATTTGCAAACTGGGAAGAGACATCTCCATTTAAAGATCCGCGCAGCTGTA	2280
Qy	2281	TGATTTTTTAAAGACGAAAGCCGAGAGGAATCTGTCTTTTCCACGCGCACTGGG	2340
Db	2281	TGATTTTTTAAAGACGAAAGCCGAGAGGAATCTGTCTTTTCCACGCGCACTGGG	2340
Qy	2341	AGACAGCAACATCTTTGTGAAAGATGGCAAGTAAAGTGGCTTTATTTGATCTTGGGAGAAG	2400
Db	2341	AGACAGCAACATCTTTGTGAAAGATGGCAAGTAAAGTGGCTTTATTTGATCTTGGGAGAAG	2400
Qy	2401	CGGAGGCGGACAAGTGGTATGACATTCGCTTCTGGCTCCGCTCGATCAGGAGGATAT	2460
Db	2401	CGGAGGCGGACAAGTGGTATGACATTCGCTTCTGGCTCCGCTCGATCAGGAGGATAT	2460
Qy	2461	CGGGGAAGACAGTATGTCGAGCTATTTTGTGACTTACTCGGGATCAAGCTGATTCGGA	2520
Db	2461	CGGGGAAGACAGTATGTCGAGCTATTTTGTGACTTACTCGGGATCAAGCTGATTCGGA	2520
Qy	2521	GAAATAAATATTTATTTTACTGGATGAATCTGTTTAGTACCTAGATGTGGCGCAACG	2580
Db	2521	GAAATAAATATTTATTTTACTGGATGAATCTGTTTAGTACCTAGATGTGGCGCAACG	2580
Qy	2581	ATGCCGGCGACAAGCAGGAGCGCACCGACTTCTTCCGCAATCAAGTGTGTTGGCTCTCAGG	2640
Db	2581	ATGCCGGCGACAAGCAGGAGCGCACCGACTTCTTCCGCAATCAAGTGTGTTGGCTCTCAGG	2640
Qy	2641	CCGAGGCCACGCAAGTATTTTGGCAAGGGTCTGCTGTTATTCGTCAGGGCAAGATTTC	2700
Db	2641	CCGAGGCCACGCAAGTATTTTGGCAAGGGTCTGCTGTTATTCGTCAGGGCAAGATTTC	2700
Qy	2701	GGATATCAAGTACGAGAGGACGGCCAGACGGCTCTACGGACCGACTTCAATTGCCGATA	2760
Db	2701	GGATATCAAGTACGAGAGGACGGCCAGACGGCTCTACGGACCGACTTCAATTGCCGATA	2760
Qy	2761	AGGTGGATTATCTGGACACCAAGGACCCAGCGGGTCAAATCAGGAATAAGGGCACATTG	2820
Db	2761	AGGTGGATTATCTGGACACCAAGGACCCAGCGGGTCAAATCAGGAATAAGGGCACATTG	2820

Qy	2821	CCCCGGCTGAGTTCGGGGCAATCCCGCAAGGAGGTTGAATGAATCGAAGTTCGACCGGA	2880
Db	2821	CCCCGGCTGAGTTCGGGGCAATCCCGCAAGGAGGTTGAATGAATCGAAGTTCGACCGGA	2880
Qy	2881	AGGCATACAGGCAAGAACTGATCGACGGGGTTTTCCGCCGAGGATCCGGAACCATCG	2940
Db	2881	AGGCATACAGGCAAGAACTGATCGACGGGGTTTTCCGCCGAGGATCCGGAACCATCG	2940
Qy	2941	CAAGCGCACCGTCAATCGTGGCCCGCGAAACCTTCCAGTCCGTCGGTTCGATGGTCC	3000
Db	2941	CAAGCGCACCGTCAATCGTGGCCCGCGCGAAACCTTCCAGTCCGTCGGTTCGATGGTCC	3000
Qy	3001	AGCAAGCTACGGCCAAAGATCGAGCGGACAGCGTGAACCTGGCTCCCCCTGCCCTCCCG	3060
Db	3001	AGCAAGCTACGGCCAAAGATCGAGCGGACAGCGTGAACCTGGCTCCCCCTGCCCTCCCG	3060
Qy	3061	CGCCATCGGCGCGCTGGAGCGTTCCGTCGTTCCGAAACAGGAGCGGAGGTTTGGCGA	3120
Db	3061	CGCCATCGGCGCGCTGGAGCGTTCCGTCGTTCCGAAACAGGAGCGGAGGTTTGGCGA	3120
Qy	3121	AGTCGATGACCATCGACCGGAGGAATATGACGACCAAGAGCGAAACCCCGCGCG	3180
Db	3121	AGTCGATGACCATCGACCGGAGGAATATGACGACCAAGAGCGAAACCCCGCGCG	3180
Qy	3181	AGGACCTGGCAAAACAGGTACAGCGGCCCAAGCAGCGCGCTTGTGAAACACACGAAGC	3240
Db	3181	AGGACCTGGCAAAACAGGTACAGCGGCCCAAGCAGCGCGCTTGTGAAACACACGAAGC	3240
Qy	3241	AGCAGATCAAGGAATGACAGCTTTCCTGTTCCGATATTGGCCCGTGGCCGACCATGC	3300
Db	3241	AGCAGATCAAGGAATGACAGCTTTCCTGTTCCGATATTGGCCCGTGGCCGACCATGC	3300
Qy	3301	GAGCGATGCCAAACAGACACGGCCCGCTTCCACCGCGCAACAGAAATCC	3360
Db	3301	GAGCGATGCCAAACAGACACGGCCCGCTTCCACCGCGCAACAGAAATCC	3360
Qy	3361	CGCGCAGGCGCTGCAAAACAAAGTCAATTTTCCACGTCAACAAAGGACGTGAAGATCACCT	3420
Db	3361	CGCGCAGGCGCTGCAAAACAAAGTCAATTTTCCACGTCAACAAAGGACGTGAAGATCACCT	3420
Qy	3421	ACACCGGCTGAGACTGCGGGCCGACGATGACGAACTGTGTGGCAGCAGGTGTTGGAT	3480
Db	3421	ACACCGGCTGAGACTGCGGGCCGACGATGACGAACTGTGTGGCAGCAGGTGTTGGAT	3480
Qy	3481	ACCGAAGCGCACCCCTATCGCGGAGCCGATCACCTTCTACGAGCTTTGCCAGG	3540
Db	3481	ACCGAAGCGCACCCCTATCGCGGAGCCGATCACCTTCTACGAGCTTTGCCAGG	3540
Qy	3541	ACCTGGGCTGTCGATCAATGGCCGATTTACAGAAAGCCGAGGAATGCTGTGCGGCC	3600
Db	3541	ACCTGGGCTGTCGATCAATGGCCGATTTACAGAAAGCCGAGGAATGCTGTGCGGCC	3600
Qy	3601	TACAGGCGCGGATGGGCTTCACTCGACCGGCTTGGGACCTGGGAATCGGTGTCG	3660
Db	3601	TACAGGCGCGGATGGGCTTCACTCGACCGGCTTGGGACCTGGGAATCGGTGTCG	3660
Qy	3661	TGCTGCACCGCTTCCGCGTCTGACCCGTGGGACCTGGGAATCGGTGTCG	3720
Db	3661	TGCTGCACCGCTTCCGCGTCTGACCCGTGGGACCTGGGAATCGGTGTCG	3720
Qy	3721	TCGACGAGGAAATCGTCTGCTGTTTGTGGCGACCACTACAGAAATTCATATGGGAGA	3780
Db	3721	TCGACGAGGAAATCGTCTGCTGTTTGTGGCGACCACTACAGAAATTCATATGGGAGA	3780
Qy	3781	AGTACCGCAAGCTGTCCCGACCGGCGGATGTTTCGACTATTTTCAGCTCCGACCGGG	3840
Db	3781	AGTACCGCAAGCTGTCCCGACCGGCGGATGTTTCGACTATTTTCAGCTCCGACCGGG	3840
Qy	3841	AGCGGTACCGCTCAAGCTCGAAACCTTCCGCTCATGTGCGGATCGGAATTCACCCCGG	3900
Db	3841	AGCGGTACCGCTCAAGCTCGAAACCTTCCGCTCATGTGCGGATCGGAATTCACCCCGG	3900
Qy	3901	TGAAGAGTGGCGCGAGCAGTTCGGGAGAGCTTGCAGAGGAGCGGCGCTGG	3960

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Db 3901 TGAAGAAAGTGGCGGACAGAGTGGCGAAGCCTGCGAAGAGTTGCGAGGCGAGCGGCTGG 3960
Qy 3961 TGAACACGCTGGGTCAATGATGACCTGGTGCATTGCAAAAGCTAGGGCTTTGTGGGT 4020
Db 3961 TGAACACGCTGGGTCAATGATGACCTGGTGCATTGCAAAAGCTAGGGCTTTGTGGGT 4020
Qy 4021 CAGTTCGGCTGGGGTTACGAGCCAGCGCTTTACTGGCAATTCCTAGGTGACGCTTT 4080
Db 4021 CAGTTCGGCTGGGGTTACGAGCCAGCGCTTTACTGGCAATTCCTAGGTGACGCTTT 4080
Qy 4081 CTGATGGCTGCCTGTATGAGTGGTGAATTTGTGCCGAGCTGCCGTCGGGGAGCTGTT 4140
Db 4081 CTGATGGCTGCCTGTATGAGTGGTGAATTTGTGCCGAGCTGCCGTCGGGGAGCTGTT 4140
Qy 4141 GGCTGGCTGGTGGCAGGATATATTGCTGTAAACAAATTTGACGCTTAGACCACTTAATA 4200
Db 4141 GGCTGGCTGGTGGCAGGATATATTGCTGTAAACAAATTTGACGCTTAGACCACTTAATA 4200
Qy 4201 ACACATTGCGGAGCTTTTAAATGTAAGTGGGCTATCCCCGGGGGATATCCATAGGCCGG 4260
Db 4201 ACACATTGCGGAGCTTTTAAATGTAAGTGGGCTATCCCCGGGGGATATCCATAGGCCGG 4260
Qy 4261 ATCTAGTAACATATGACACGGCGCGGATAATTTATCTAGTTTGGCGCTATATTTTG 4320
Db 4261 ATCTAGTAACATATGACACGGCGCGGATAATTTATCTAGTTTGGCGCTATATTTTG 4320
Qy 4321 TTTTCTATCCGCTATTAATGTAATTTGCGGAGCTCTAATCATATAAAACCCATCTCAT 4380
Db 4321 TTTTCTATCCGCTATTAATGTAATTTGCGGAGCTCTAATCATATAAAACCCATCTCAT 4380
Qy 4381 AATAACGTCATGCAATACATGTTTAAATTTATACATGCTTAACGTAATTCACAGAAATAT 4440
Db 4381 AATAACGTCATGCAATACATGTTTAAATTTATACATGCTTAACGTAATTCACAGAAATAT 4440
Qy 4441 ATGATAATCATGCAAGACCGCGCAAGGATTCATCTTAAGAAACTTTATTCGCAAAATG 4500
Db 4441 ATGATAATCATGCAAGACCGCGCAAGGATTCATCTTAAGAAACTTTATTCGCAAAATG 4500
Qy 4501 TTTTGAACGATCGTTTGTGCGAGCTATGGGCCCGA 4533
Db 4501 TTTTGAACGATCGTTTGTGCGAGCTATGGGCCCGA 4533
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RESULT 10
US-09-845-064-8
; Sequence 8, Application US/09845064
; Publication No. US20030175976A1
; GENERAL INFORMATION:
; APPLICANT: MERISTEM THERAPEUTICS
; TITLE OF INVENTION: CLEAN SYNTHETIC VECTORS, PLASMIDS, TRANSGENIC PLANTS
; TITLE OF INVENTION: AND PLANT PARTS CONTAINING SAID VECTORS, AND THEIR
; TITLE OF INVENTION: METHODS OF PRODUCTION
; FILE REFERENCES: SynVec1
; CURRENT APPLICATION NUMBER: US/09/845,064
; CURRENT FILING DATE: 2001-04-27
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 8
; LENGTH: 6767
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Plasmid
; OTHER INFORMATION: pMR11175
; FEATURE:
; NAME/KEY: rep_origin
; LOCATION: (1)..(654)
; OTHER INFORMATION: Origin of replication ori RK2
; FEATURE:
; NAME/KEY: rep_origin
; LOCATION: (655)..(1263)
; OTHER INFORMATION: Origin of replication ori Colei
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; FEATURE:
; NAME/KEY: gene
; LOCATION: (1264)..(2603)
; OTHER INFORMATION: NPT III gene coding for neomycin
; OTHER INFORMATION: phosphotransferase and kanamycin resistance
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (2604)..(4098)
; OTHER INFORMATION: TrfA locus from RK2 coding for two proteins, p285
; OTHER INFORMATION: and p382, enabling the increase in the rate of
; OTHER INFORMATION: replication
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (4106)..(4271)
; OTHER INFORMATION: T-DNA left border
; FEATURE:
; NAME/KEY: terminator
; LOCATION: (4272)..(4559)
; OTHER INFORMATION: No. US20030175976Alaline synthetase terminator
; FEATURE:
; NAME/KEY: gene
; LOCATION: (4559)..(5556)
; OTHER INFORMATION: NPT II gene coding for neomycin phosphotransferase
; OTHER INFORMATION: and kanamycin resistance
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (5557)..(5771)
; OTHER INFORMATION: No. US20030175976Alaline synthetase promoter
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (5771)..(5830)
; OTHER INFORMATION: MCS multiple cloning site
; FEATURE:
; NAME/KEY: polyA_signal
; LOCATION: (5830)..(6560)
; OTHER INFORMATION: Poly A from 35S ribosome
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (6560)..(6587)
; OTHER INFORMATION: MCS multiple cloning site
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (6587)..(6760)
; OTHER INFORMATION: T-DNA right border
; US-09-845-064-8
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Query Match 94.3%; Score 4531.4; DB 10; Length 6767;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4532; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCGGGCTGTTGCCCTCGCGCTGGGCTGGGCGCGCTCTATGSCCTTGCAACGCCGCGAG 60
Db 1 CCGGGCTGTTGCCCTCGCGCTGGGCTGGGCGCGCTCTATGSCCTTGCAACGCCGCGAG 60

Qy 61 AAACGCGTCGAAGCGCTGTGCGAGACACCGCGCGCGCGGCTTGTGGATACCTCGCGG 120
Db 61 AAACGCGTCGAAGCGCTGTGCGAGACACCGCGCGCGCGGCTTGTGGATACCTCGCGG 120

Qy 121 AAAAATTGGCCCTCACTGACAGATGAGGGCGGACGTTGACACTTGAGGGGCGGACTCAC 180
Db 121 AAAAATTGGCCCTCACTGACAGATGAGGGCGGACGTTGACACTTGAGGGGCGGACTCAC 180

Qy 181 CCGGCGCGCGGTTGACAGATGAGGGCGGAGCTCGATTTCCGCGGCGAGCTGGAGCTGGC 240
Db 181 CCGGCGCGCGGTTGACAGATGAGGGCGGAGCTCGATTTCCGCGGCGAGCTGGAGCTGGC 240

Qy 241 CAGCCTCGCAAAATCGCGGAAAAACCGCTGATTTTACCGAGTTTCCACAGATGATGTGA 300
Db 241 CAGCCTCGCAAAATCGCGGAAAAACCGCTGATTTTACCGAGTTTCCACAGATGATGTGA 300

Qy 301 CAAAGCTGGGGATAAGTGCCTCGCGGTATTGACACTTTGAGGGGCGGAGTACTACAGAT 360
Db 301 CAAAGCTGGGGATAAGTGCCTCGCGGTATTGACACTTTGAGGGGCGGAGTACTACAGAT 360
```

Qy	361	GAGGGCGCATCTTTCACACTTGGAGGCGAGAGTGTGACAGATGAGGGCGCACCTAT	420
Db	361	GAGGGCGCATCTTTCACACTTGGAGGCGAGAGTGTGACAGATGAGGGCGCACCTAT	420
Qy	421	TGACATTTGAGGGGCTGTCCACAGGCGAGAAATCCAGCATTTGCAAGGGTTTCGGCCCGT	480
Db	421	TGACATTTGAGGGGCTGTCCACAGGCGAGAAATCCAGCATTTGCAAGGGTTTCGGCCCGT	480
Qy	481	TTTTGGCGCACCGGTAACTGTCTTTTAACTGTCTTTTAACTTTTAACTTTTAACTTTG	540
Db	481	TTTTGGCGCACCGGTAACTGTCTTTTAACTGTCTTTTAACTTTTAACTTTTAACTTTG	540
Qy	541	TTTTTAACCAAGGCTGCGCCCTGTGCGGTGACCGCGACCGCGAAGGGGGTGC	600
Db	541	TTTTTAACCAAGGCTGCGCCCTGTGCGGTGACCGCGACCGCGAAGGGGGTGC	600
Qy	601	CTTCTCGAAACCTCCCGAAAGGTATGCGGTGTGAATACCGCACAGATCGTAAAGAGA	660
Db	601	CTTCTCGAAACCTCCCGAAAGGTATGCGGTGTGAATACCGCACAGATCGTAAAGAGA	660
Qy	661	AAATACCGCATCAGGCGCTCTTTCGGCTTCTCGCTCACTGACTCGCTGCGCTCGGTCGTT	720
Db	661	AAATACCGCATCAGGCGCTCTTTCGGCTTCTCGCTCACTGACTCGCTGCGCTCGGTCGTT	720
Qy	721	CGGCTGCGGAGCGGTATCAGCTCACTCAAAGCGGTATACGTTATCCACAGATCA	780
Db	721	CGGCTGCGGAGCGGTATCAGCTCACTCAAAGCGGTATACGTTATCCACAGATCA	780
Qy	781	GGGGATAACCGAGAAAGAACATGTAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAA	840
Db	781	GGGGATAACCGAGAAAGAACATGTAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAA	840
Qy	841	AAGCCCGGTTGCTGGCGTTTTTCCATAGGCTCCGCCCTCGCTGACGAGCATCAAAAAT	900
Db	841	AAGCCCGGTTGCTGGCGTTTTTCCATAGGCTCCGCCCTCGCTGACGAGCATCAAAAAT	900
Qy	901	CGAGCTCAAGTCAGAGGTGCGAAACCGGACAGACTATAAGATACCGAGGCTTTCCC	960
Db	901	CGAGCTCAAGTCAGAGGTGCGAAACCGGACAGACTATAAGATACCGAGGCTTTCCC	960
Qy	961	CCTGGAAGCTCCCTGCTGCGCTCTCTGTTCGACCCCTGCGGCTTACCGGATACCTGTCC	1020
Db	961	CCTGGAAGCTCCCTGCTGCGCTCTCTGTTCGACCCCTGCGGCTTACCGGATACCTGTCC	1020
Qy	1021	GCCTTTCTCCCTTCGGGAAGCGTGGCGCTTCTCATAGCTCACGCTGTAGGTATCTCAGT	1080
Db	1021	GCCTTTCTCCCTTCGGGAAGCGTGGCGCTTCTCATAGCTCACGCTGTAGGTATCTCAGT	1080
Qy	1081	TCGGTGTAGGTGCTTCGCTCCAAGCTGGGCTGTGTCACGAAACCCCGGTCAGCCCGAC	1140
Db	1081	TCGGTGTAGGTGCTTCGCTCCAAGCTGGGCTGTGTCACGAAACCCCGGTCAGCCCGAC	1140
Qy	1141	CGCTGCGCTTATCCGGTAACTATCTGCTTGTAGTCCAAACCGGTTAAGACAGACTATCG	1200
Db	1141	CGCTGCGCTTATCCGGTAACTATCTGCTTGTAGTCCAAACCGGTTAAGACAGACTATCG	1200
Qy	1201	CCACTGCGAGCGCTTCTTACCATAATCCGCGATAAACCCAGCGAAACATTTGAGGTGAT	1260
Db	1201	CCACTGCGAGCGCTTCTTACCATAATCCGCGATAAACCCAGCGAAACATTTGAGGTGAT	1260
Qy	1261	AGGTAAAGATTATACGAGGTATGAACAGAGAAATTTGACCTTTTACAGAAATTTACTATGA	1320
Db	1261	AGGTAAAGATTATACGAGGTATGAACAGAGAAATTTGACCTTTTACAGAAATTTACTATGA	1320
Qy	1321	AGCCGCCATTTTAAAGCTACCAAGACGAAGAGATGAAGAGGATGAGGAGGAGATTTG	1380
Db	1321	AGCCGCCATTTTAAAGCTACCAAGACGAAGAGATGAAGAGGATGAGGAGGAGATTTG	1380
Qy	1381	CTTTGAATATATGACAAATCTGTATAGATTAATACATCTTTTATATAGAAAGATATCGCG	1440
Db	1381	CTTTGAATATATGACAAATCTGTATAGATTAATACATCTTTTATATAGAAAGATATCGCG	1440

Qy	1441	TATGTAAAGATTTTCAGGGGCAAGGCATAGGCAGCGCGTTATCAATATATCTATAGAAT	1500
Db	1441	TATGTAAAGATTTTCAGGGGCAAGGCATAGGCAGCGCGTTATCAATATATCTATAGAAT	1500
Qy	1501	GGCAAAAGCATAAAACTTGCATGGAATAATGCTTGAACCCAGGACAATAACCTTATAG	1560
Db	1501	GGCAAAAGCATAAAACTTGCATGGAATAATGCTTGAACCCAGGACAATAACCTTATAG	1560
Qy	1561	CTTGTAAATTTTACCAAAATTTGTTTCAAAATCGGCTCCGTCGATACTATGTTATACG	1620
Db	1561	CTTGTAAATTTTACCAAAATTTGTTTCAAAATCGGCTCCGTCGATACTATGTTATACG	1620
Qy	1621	CCAACTTTGAAAACTTTTGAAGAGCTGTTTTCTGGTATTTTAAAGTTTTTAAAGTCAA	1680
Db	1621	CCAACTTTGAAAACTTTTGAAGAGCTGTTTTCTGGTATTTTAAAGTTTTTAAAGTCAA	1680
Qy	1681	GGAACTGTAATTTGGAGTTTCGTTCTTGTATTAATAGTCTTCTGGGTATCTTTAAATACT	1740
Db	1681	GGAACTGTAATTTGGAGTTTCGTTCTTGTATTAATAGTCTTCTGGGTATCTTTAAATACT	1740
Qy	1741	GTAGAAAGAGGAAGAAATAAATGCTAAATGGAATATCACCGAAATGAAAAA	1800
Db	1741	GTAGAAAGAGGAAGAAATAAATGCTAAATGGAATATCACCGAAATGAAAAA	1800
Qy	1801	ACTGTATCGAAAAATACCGCTGCTAAAGATACGGAAGGAATGCTCTCTGCTAAGGTATA	1860
Db	1801	ACTGTATCGAAAAATACCGCTGCTAAAGATACGGAAGGAATGCTCTCTGCTAAGGTATA	1860
Qy	1861	TAACTGTGGGAGAAAAATGAAAACTATATTTTAAAAATGACGGAAGCGGTATTAAGG	1920
Db	1861	TAACTGTGGGAGAAAAATGAAAACTATATTTTAAAAATGACGGAAGCGGTATTAAGG	1920
Qy	1921	GACCACTATGATGTGGAACGGGAAGGACATGATGCTATGCTCGAGGAAGGCTGCC	1980
Db	1921	GACCACTATGATGTGGAACGGGAAGGACATGATGCTATGCTCGAGGAAGGCTGCC	1980
Qy	1981	TGTTTCAAAAGGCTCCTGCATCTTCAACGGCATGATGGCTGGAGCAATCTGCTCATGAGTGA	2040
Db	1981	TGTTTCAAAAGGCTCCTGCATCTTCAACGGCATGATGGCTGGAGCAATCTGCTCATGAGTGA	2040
Qy	2041	GGCCGATGCGCTCTTGTGCTGGAAGAGTATGAAGATGAACAAAGCCCTGAAAAAGATTAT	2100
Db	2041	GGCCGATGCGCTCTTGTGCTGGAAGAGTATGAAGATGAACAAAGCCCTGAAAAAGATTAT	2100
Qy	2101	CGAGCTGTATGCGGAGTGCATCAGGCTCTTCACTCCATCGACATATCGAGTTGTCCTTA	2160
Db	2101	CGAGCTGTATGCGGAGTGCATCAGGCTCTTCACTCCATCGACATATCGAGTTGTCCTTA	2160
Qy	2161	TACGAATAGCTTAGACAGCGCGCTTAGCCGAATTTGGATTACTTACTGAATAACGATCTGGC	2220
Db	2161	TACGAATAGCTTAGACAGCGCGCTTAGCCGAATTTGGATTACTTACTGAATAACGATCTGGC	2220
Qy	2221	CGATGTGGAATTCGAAACCTGGGAAGAGACATCCATTTTAAAGATCCCGCGAGCTGTGA	2280
Db	2221	CGATGTGGAATTCGAAACCTGGGAAGAGACATCCATTTTAAAGATCCCGCGAGCTGTGA	2280
Qy	2281	TGATTTTTHAAGACGGAAGCCCGAAGAGGAACCTGCTTTTCCACCGCGACCTGGG	2340
Db	2281	TGATTTTTHAAGACGGAAGCCCGAAGAGGAACCTGCTTTTCCACCGCGACCTGGG	2340
Qy	2341	AGACAGCAACATCTTTGTGAAAGATGGCAAGTAAAGTGGCTTTTATTTGATCTTGGGAGAAG	2400
Db	2341	AGACAGCAACATCTTTGTGAAAGATGGCAAGTAAAGTGGCTTTTATTTGATCTTGGGAGAAG	2400
Qy	2401	CGGACGGCGGACAAGTGGTATGACATTTGCTTCTGCGTCCGCTCGATCAGGAGGATAT	2460
Db	2401	CGGACGGCGGACAAGTGGTATGACATTTGCTTCTGCGTCCGCTCGATCAGGAGGATAT	2460
Qy	2461	CGGGGAAGACATGCTCGAGCTATTTTGTACTTACTCGGGATCAAGCTCTGATTCGGA	2520
Db	2461	CGGGGAAGACATGCTCGAGCTATTTTGTACTTACTCGGGATCAAGCTCTGATTCGGA	2520
Qy	2521	GAATAAAAAATATATATTTTACTGGATGAATTTGTTTTTAGTACCTAGATGTGGCGCAACG	2580

Db 2521 GAAAAATAAATATATATATTTTACTGATGAATTTTGTAGTACCTAGATGTGCGCAACG 2580  
Qy 2581 ATCCCGCGCAAGCAGGAGCGCACCGACTTCTTCGCGCATCAAGTGTTTTGGCTCTCAGG 2640  
Db 2581 ATCCCGCGCAAGCAGGAGCGCACCGACTTCTTCGCGCATCAAGTGTTTTGGCTCTCAGG 2640  
Qy 2641 CCAGAGGCCCAACGCAAGTATTTTGGGCAAGGGGTGCTGTGTAATTCGTGCGAGGCAAGATTC 2700  
Db 2641 CCAGAGGCCCAACGCAAGTATTTTGGGCAAGGGGTGCTGTGTAATTCGTGCGAGGCAAGATTC 2700  
Qy 2701 GGAATACCAAGTACGAGAGGAGCGCGACGCTCTACGGGACCGACTTCATTGCGCGATA 2760  
Db 2701 GGAATACCAAGTACGAGAGGAGCGCGACGCTCTACGGGACCGACTTCATTGCGCGATA 2760  
Qy 2761 AGGTGGAATATCTGGACACCAAGGCAACGAGCGGGGTCAATATCAGGAATAGGGCAATTCG 2820  
Db 2761 AGGTGGAATATCTGGACACCAAGGCAACGAGCGGGGTCAATATCAGGAATAGGGCAATTCG 2820  
Qy 2821 CCCCGCGGTGAGTCCGGGCAATCCCGCAAGGAGGGTGAATGAATCGGACCGGA 2880  
Db 2821 CCCCGCGGTGAGTCCGGGCAATCCCGCAAGGAGGGTGAATGAATCGGACCGGA 2880  
Qy 2881 AGGCATACAGGCAAGCACTGATCGACGCGGGGTTTCCGCGGAGGATGCCGAAACCATCG 2940  
Db 2881 AGGCATACAGGCAAGCACTGATCGACGCGGGGTTTCCGCGGAGGATGCCGAAACCATCG 2940  
Qy 2941 CAAAGCCGACCGTATCGTGGCGGCGCCCGGAAACCTTCCAGTCCGTCGGGTCGATGGTCC 3000  
Db 2941 CAAAGCCGACCGTATCGTGGCGGCGCCCGGAAACCTTCCAGTCCGTCGGGTCGATGGTCC 3000  
Qy 3001 AGCAAGCTACGGCAAGATCGAGCGGACACGCGTGAACCTGCGCTCCCTCGCCCTCGCCG 3060  
Db 3001 AGCAAGCTACGGCAAGATCGAGCGGACACGCGTGAACCTGCGCTCCCTCGCCCTCGCCG 3060  
Qy 3061 CGCCATCGCGCGCGTGGAGCGTTCGCTCGTCTCGAACAAGGAGCGGCAAGTGTGGCGA 3120  
Db 3061 CGCCATCGCGCGCGTGGAGCGTTCGCTCGTCTCGAACAAGGAGCGGCAAGTGTGGCGA 3120  
Qy 3121 AGTCGATGACATCGACACGCGAGGAACTATGACGACCAAGAGCGGCAAGAAACCGCGCG 3180  
Db 3121 AGTCGATGACATCGACACGCGAGGAACTATGACGACCAAGAGCGGCAAGAAACCGCGCG 3180  
Qy 3181 AGGACCTGGCAAAACAGGTGAGCGAGGCAAGCAGCGCGGTTGCTGAAACACACGAAAGC 3240  
Db 3181 AGGACCTGGCAAAACAGGTGAGCGAGGCAAGCAGCGCGGTTGCTGAAACACACGAAAGC 3240  
Qy 3241 AGCAGATCAAGGAAATGCAAGTTCCTTGTGTAATTCGCGGTCGCGGCGGACACGATGC 3300  
Db 3241 AGCAGATCAAGGAAATGCAAGTTCCTTGTGTAATTCGCGGTCGCGGTCGCGGACACGATGC 3300  
Qy 3301 GAGCGATGCCAAACGACACGCGCGCTCTGCGCTGTTCCACGCGCGCAACAGAAATCC 3360  
Db 3301 GAGCGATGCCAAACGACACGCGCGCTCTGCGCTGTTCCACGCGCGCAACAGAAATCC 3360  
Qy 3361 CGCGCAGGCGCTGCAAAACAAGTCAATTTTCAAGTCAACAGGACGTCGAGATCACCT 3420  
Db 3361 CGCGCAGGCGCTGCAAAACAAGTCAATTTTCAAGTCAACAGGACGTCGAGATCACCT 3420  
Qy 3421 ACACCGCGCTGAGCTCGCGGCGCGACGATACGAACTGTTGTCGAGCAGGTTGCGAGT 3480  
Db 3421 ACACCGCGCTGAGCTCGCGGCGCGACGATACGAACTGTTGTCGAGCAGGTTGCGAGT 3480  
Qy 3481 ACAGGAGCGCACCCCTATCGGCGGCGGATCACTTCAGTTCACGAGCTTTGCGAGG 3540  
Db 3481 ACAGGAGCGCACCCCTATCGGCGGCGGATCACTTCAGTTCACGAGCTTTGCGAGG 3540  
Qy 3541 ACCTGGCTGCTGATCAATGGCGGTTTACAGAGGCGGAGGATGCTGTCGCGCC 3600  
Db 3541 ACCTGGCTGCTGATCAATGGCGGTTTACAGAGGCGGAGGATGCTGTCGCGCC 3600  
Qy 3601 TACAGGCGAGCGGATGGGCTTACGTCGCGCGGTTGGGCACTTGGGAATCGGTGCGC 3660

Db 3601 TACAGCGAGCGGATGGGCTTCACTCCGACCGCGTTGGGCACTCTGGAAATCGGTGTCG 3660  
Qy 3661 TGTCTCACCGCTTCCGCGTCTGGAGCCGCTGGCAAGAAACGTCCTCCCTGTCAGAGTCTCTGA 3720  
Db 3661 TGTCTCACCGCTTCCGCGTCTGGAGCCGCTGGCAAGAAACGTCCTCCCTGTCAGAGTCTCTGA 3720  
Qy 3721 TCGAGAGGAAATCGTGTGCTGTTTGTCTGGGCAACCTACACGAAATTCATATGGGAGA 3780  
Db 3721 TCGAGAGGAAATCGTGTGCTGTTTGTCTGGGCAACCTACACGAAATTCATATGGGAGA 3780  
Qy 3781 AGTACCGCAAGCTGTCCGCGAGCGCCGAGCGATGTTTCAGCTTCGACCCGGG 3840  
Db 3781 AGTACCGCAAGCTGTCCGCGAGCGCCGAGCGATGTTTCAGCTTCGACCCGGG 3840  
Qy 3841 AGCCGTACCCGCTCAAGCTGGAAACCTTCCGCTCATGTGCGGATCGGATTCACCCCGG 3900  
Db 3841 AGCCGTACCCGCTCAAGCTGGAAACCTTCCGCTCATGTGCGGATCGGATTCACCCCGG 3900  
Qy 3901 TGAAGAAGTGGCGGAGCGAGGTCGGGAAAGCTCGGAAAGTTCGAGGAGCGGCGCTGG 3960  
Db 3901 TGAAGAAGTGGCGGAGCGAGGTCGGGAAAGCTCGGAAAGTTCGAGGAGCGGCGCTGG 3960  
Qy 3961 TGGAAACACCCCTGGGTCAATGATGACCTGCTGATGCAAACTGAGGCGCTTGTGGGT 4020  
Db 3961 TGGAAACACCCCTGGGTCAATGATGACCTGCTGATGCAAACTGAGGCGCTTGTGGGT 4020  
Qy 4021 CAGTTCCGCTGGGGTTCAGCAGCGAGCGCTTACTGGCATTTCTAGCTTGACGCTCTT 4080  
Db 4021 CAGTTCCGCTGGGGTTCAGCAGCGAGCGCTTACTGGCATTTCTAGCTTGACGCTCTT 4080  
Qy 4081 CTGATGGGCTGCTGATCGAGTGTGATTTTGTGCGGAGTCCCGTGGGAGCTGTT 4140  
Db 4081 CTGATGGGCTGCTGATCGAGTGTGATTTTGTGCGGAGTCCCGTGGGAGCTGTT 4140  
Qy 4141 GSCTGCTGCTGGCAGGATATATTGCTGTGTAACAAATGACGCTAGACAACTTAATA 4200  
Db 4141 GSCTGCTGCTGGCAGGATATATTGCTGTGTAACAAATGACGCTAGACAACTTAATA 4200  
Qy 4201 ACACATTCGCGGAGCTTTTAAATGATGCTGCTATCCCGGGGATATCCATAGGCGCG 4260  
Db 4201 ACACATTCGCGGAGCTTTTAAATGATGCTGCTATCCCGGGGATATCCATAGGCGCG 4260  
Qy 4261 ATCTAGTAACTAATGACACCGCGCGATAATTTATCTAGTTTCGCGCTATATTTTG 4320  
Db 4261 ATCTAGTAACTAATGACACCGCGCGATAATTTATCTAGTTTCGCGCTATATTTTG 4320  
Qy 4321 TTTTCTATCGCTATTAATGATGATTTGCGGAGCTCTAATCATATAAAACCCATCTCAT 4380  
Db 4321 TTTTCTATCGCTATTAATGATGATTTGCGGAGCTCTAATCATATAAAACCCATCTCAT 4380  
Qy 4381 AATAACGTCATGCTTACATGTTAATTTATGCTTAACGTAATTCACAGAAATAT 4440  
Db 4381 AATAACGTCATGCTTACATGTTAATTTATGCTTAACGTAATTCACAGAAATAT 4440  
Qy 4441 ATGATAATCATCGCAAGACCGGCAACAGGATTCATTTTAAGAAACTTTATGCCAAATG 4500  
Db 4441 ATGATAATCATCGCAAGACCGGCAACAGGATTCATTTTAAGAAACTTTATGCCAAATG 4500  
Qy 4501 TTTGAACGATCGTTCGTCGAGCTATGGGCGCA 4533  
Db 4501 TTTGAACGATCGTTCGTCGAGCTATGGGCGCA 4533

## RESULT 11

US-09-845-064-9  
; Sequence 9, Application US/09845064  
; Publication No. US20030175976A1  
; GENERAL INFORMATION:  
; APPLICANT: MERISTEM THERAPEUTICS  
; TITLE OF INVENTION: CLEAN SYNTHETIC VECTORS, PLASMIDS, TRANSGENIC PLANTS  
; TITLE OF INVENTION: AND PLANT PARTS CONTAINING SAID VECTORS, AND THEIR  
; TITLE OF INVENTION: METHODS OF PRODUCTION  
; FILE REFERENCE: SynVec1





Db	1141		CGCTGCGCTTATCCGGTAACTATCGTCTTGAGTCCAAACCGGTAAACACGACTTATCG	1201
Qy	1201	CCACTGGCAGCAGCTTCTACCAATAATCCGCGATAAACCAGCGAAACCATTTGAGGTGAT	1260	1261
Db	1201	CCACTGGCAGCAGCTTCTACCAATAATCCGCGATAAACCAGCGAAACCATTTGAGGTGAT	1260	1261
Qy	1261	AGGTAAGATTATACCGAGGTATGAAACGAGAAATGGACCTTTACAGAAATTAATCTATGA	1320	1321
Db	1261	AGGTAAGATTATACCGAGGTATGAAACGAGAAATGGACCTTTACAGAAATTAATCTATGA	1320	1321
Qy	1321	AGGCCCATATTTAAAGCTTACCAAGACGAAGAGGATGAAGAGATGAGAGCGAGATTG	1380	1381
Db	1321	AGGCCCATATTTAAAGCTTACCAAGACGAAGAGGATGAAGAGATGAGAGCGAGATTG	1380	1381
Qy	1381	CTTTGAATATATTGACAATACTGATAAGATAATAACATCTTTTATATAGAAGATATCGCG	1440	1441
Db	1381	CTTTGAATATATTGACAATACTGATAAGATAATAACATCTTTTATATAGAAGATATCGCG	1440	1441
Qy	1441	TATGTAAGGATTTTCAGGGGCAAGGCATAGGCAGCGCTTATCAATATATCTATAGAAT	1500	1501
Db	1441	TATGTAAGGATTTTCAGGGGCAAGGCATAGGCAGCGCTTATCAATATATCTATAGAAT	1500	1501
Qy	1501	GGGCAAGCATAAAACCTTGCATGGACTAATGCTTGAACCCAGGCAATAAACCCTTATAG	1560	1561
Db	1501	GGGCAAGCATAAAACCTTGCATGGACTAATGCTTGAACCCAGGCAATAAACCCTTATAG	1560	1561
Qy	1561	CTTGTAATCTTACCAAAATTTGCTTTCAAAATCGGCTCCGTCGATACATGTTATACG	1620	1621
Db	1561	CTTGTAATCTTACCAAAATTTGCTTTCAAAATCGGCTCCGTCGATACATGTTATACG	1620	1621
Qy	1621	CCAACTTTGAAAACAACTTTGAAAAGCTGTGTTCTGTTATTTAAAGTTTAAAGTGC	1680	1681
Db	1621	CCAACTTTGAAAACAACTTTGAAAAGCTGTGTTCTGTTATTTAAAGTTTAAAGTGC	1680	1681
Qy	1681	GGAAACAGTGAAATTGGAGTTGCTCTTGTTTAAATTAAGCTTCTGCGGTATCTTTAAAT	1740	1741
Db	1681	GGAAACAGTGAAATTGGAGTTGCTCTTGTTTAAATTAAGCTTCTGCGGTATCTTTAAAT	1740	1741
Qy	1741	GTGAAAGAGGAGGAGAAATAATAATGGCTTAAATCAGAAATCAACCGGAAATGGA	1800	1801
Db	1741	GTGAAAGAGGAGGAGAAATAATAATGGCTTAAATCAGAAATCAACCGGAAATGGA	1800	1801
Qy	1801	ACTGATCGAAAAATACCGCTCGCTTAAAGATACGGAAGGAATGTCCTGCTAAAGTATA	1860	1861
Db	1801	ACTGATCGAAAAATACCGCTCGCTTAAAGATACGGAAGGAATGTCCTGCTAAAGTATA	1860	1861
Qy	1861	TAACTCGGTGGAGAAAATGAAACCTTATATTTAAAAATCAGGACACGCGGTATAAAG	1920	1921
Db	1861	TAACTCGGTGGAGAAAATGAAACCTTATATTTAAAAATCAGGACACGCGGTATAAAG	1920	1921
Qy	1921	GACCACCTATGATGTGAAACGGGAAAGGACATGCTATGCTCGGAAGGAAGCTGCC	1980	1981
Db	1921	GACCACCTATGATGTGAAACGGGAAAGGACATGCTATGCTCGGAAGGAAGCTGCC	1980	1981
Qy	1981	TGTTCCAAAGTCTCGACCTTGAAACGGCATGATGGCTGGAGCAATCTGCTCATGAGTGA	2040	2041
Db	1981	TGTTCCAAAGTCTCGACCTTGAAACGGCATGATGGCTGGAGCAATCTGCTCATGAGTGA	2040	2041
Qy	2041	GGCCGATGGCGTCTTTGCTCGGAAGAGTATGAAGATGAACAAAGCCCTGAAAGATTAT	2100	2101
Db	2041	GGCCGATGGCGTCTTTGCTCGGAAGAGTATGAAGATGAACAAAGCCCTGAAAGATTAT	2100	2101
Qy	2101	CGAGCTGATGCGGAGTGCAATCAGGCTTTTCACTCCATCGATATCGGATGTCCTTA	2160	2161
Db	2101	CGAGCTGATGCGGAGTGCAATCAGGCTTTTCACTCCATCGATATCGGATGTCCTTA	2160	2161
Qy	2161	TACGAATAGCTTAGACAGCGCTTAGCCGAATTTGGATTACTTACTGAATAACGATCTGCC	2220	2221
Db	2161	TACGAATAGCTTAGACAGCGCTTAGCCGAATTTGGATTACTTACTGAATAACGATCTGCC	2220	2221
Qy	2221	CGATGTGGATTGCGAAACCTGGGAAGAGACACTCCATTTTAAAGATCCCGCGAGCTGTA	2280	

2221	CGATGTGGATTGCGAAAACTGGGAAGAGACACTCATTTTAAAGATCTCCGCGAGCTGTA	2288
2281	TGATTTTTTAAAGACGAAAAAGCCGAAAGAGGAACCTGTCTTTTCCACGGCGACCTGGG	2340
2281	TGATTTTTTAAAGACGAAAAAGCCGNAAGGAACTTGCTTTTCCACGGCGACCTGGG	2340
2341	AGACAGCAACATCTTTGTGAAAGATGCGAAAGTAAGTGCGCTTTATTGATCTTGGGAGAAG	2400
2341	AGACAGCAACATCTTTGTGAAAGATGCGAAAGTAAGTGCGCTTTATTGATCTTGGGAGAAG	2400
2401	CGCAGGGCGGACAAAGTGGTATGACATTCGCTTCTCGCTCCGCTCCGATCAGGCGAGGATAT	2460
2401	CGGCGAGGCGGACAAAGTGGTATGACATTCGCTTCTCGCTCCGCTCCGATCAGGCGAGGATAT	2460
2461	CGGGGAAGAACAGTATGTCGAGCTATTTTTTTGACTTTACTGGGGATCAAGCCTCATTTGGGA	2520
2461	CGGGGAAGAACAGTATGTCGAGCTATTTTTTTGACTTTACTGGGGATCAAGCCTCATTTGGGA	2520
2521	GAAAAATAAATATATATTTTACTGATGAATTTGTTTTTACTCTAGATGTGCGGCAACG	2580
2521	GAAAAATAAATATATATTTTACTGATGAATTTGTTTTTACTCTAGATGTGCGGCAACG	2580
2581	ATCCGCGCAGACGAGGAGCGCACCGACTTCTTCGCGCATCAAGTCTTTTGGCTCTCAGG	2640
2581	ATCCGCGCAGACGAGGAGCGCACCGACTTCTTCGCGCATCAAGTCTTTTGGCTCTCAGG	2640
2641	CCGAGGCCACGGCAAGTATTTTCGGCAAGGGGTCTGCTGATTTCTGTCAGGGCAAGATTC	2700
2641	CCGAGGCCACGGCAAGTATTTTCGGCAAGGGGTCTGCTGATTTCTGTCAGGGCAAGATTC	2700
2701	GGAAATACCAAGTACGAGAAAGGACGGCGACAGCGGTCTACGGGACCGACTTCATTTGCCGATA	2760
2701	GGAAATACCAAGTACGAGAAAGGACGGCGACAGCGGTCTACGGGACCGACTTCATTTGCCGATA	2760
2761	AGGTGGATTTATCTGGACACCAAGGCCACGCGGGTCAAAATCAGGAAATAGGCGCACATTG	2820
2761	AGGTGGATTTATCTGGACACCAAGGCCACGAGCGGGTCAAAATCAGGAAATAGGCGCACATTG	2820
2821	CCCCGGCGTCAGTTCGGGGCAATCCCGCAAGAGGGGTGAATGAATCGGACGTTTTCACCGGA	2880
2821	CCCCGGCGTCAGTTCGGGGCAATCCCGCAAGAGGGGTGAATGAATCGGACGTTTTCACCGGA	2880
2881	AGGCATACAGGCAAGAACTGATCGACGCGGGGTTTTCCGCGAGGATGCGGAAACCATCG	2940
2881	AGGCATACAGGCAAGAACTGATCGACGCGGGGTTTTCCGCGAGGATGCGGAAACCATCG	2940
2941	CAAGCGCACCGTCTATCGTTCGCGCCCGCGGAAACCTTTCAGTCCGTCGCTCGATGGTCC	3000
2941	CAAGCGCACCGTCTATCGTTCGCGCCCGCGGAAACCTTTCAGTTCGCTCGATGGTCC	3000
3001	AGCAAGCTACGGCCAAAGATCGAGCGCGACAGCGTCAAACTTGGCTCCCTTCGCTCCCGG	3060
3001	AGCAAGCTACGGCCAAAGATCGAGCGCGACAGCGTCAAACTTGGCTCCCTTCGCTCCCGG	3060
3061	CGCCATCGGCCCGCTGGAGCGTTTCGCGTCTCGAAACAGGAGGCGGAGGTTTGGCGGA	3120
3061	CGCCATCGGCCCGCTGGAGCGTTTCGCGTCTCGAAACAGGAGGCGGAGGTTTGGCGGA	3120
3121	AGTCGATGACCATTCGACACGCGAGGAACCTATGACACCAAGAAAGCGGAAAAACCGCCGGG	3180
3121	AGTCGATGACCATTCGACACGCGAGGAACCTATGACACCAAGAAAGCGGAAAAACCGCCGGG	3180
3181	AGGACCTGGCAAAACAGGTCAGCGAGGCCAAGCAGCGCCGCTTGCTGTAACACACCAAGC	3240
3181	AGGACCTGGCAAAACAGGTCAGCGAGGCCAAGCAGCGCCGCTTGCTGTAACACACCAAGC	3240
3241	AGCAGATCAAGGAATTCAGCTTTTCTGTTTCGATATTCGCGCGTGGCGCGCACGATGC	3300
3241	AGCAGATCAAGGAATTCAGCTTTTCTGTTTCGATATTCGCGCGTGGCGCGCACGATGC	3300
3301	GAGCGATGCAAAACGACACGCGCCGCTCTGCTTTCGATATTCGCGCGTGGCGCGCACGATGC	3360
3301	GAGCGATGCAAAACGACACGCGCCGCTCTGCTTTCGATATTCGCGCGTGGCGCGCACGATGC	3360

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QY 3361 CGCGGAGGCGCTGCRAAAACAAGTCAATTTTCCACGTCACAAGGACGTGAAGATCACCT 3420
Db 3361 CGCGGAGGCGCTGCRAAAACAAGTCAATTTTCCACGTCACAAGGACGTGAAGATCACCT 3420
QY 3421 ACACCGCGTCGAGCTCGCGGCGCACGATGACGAACTGGTGTGCGCAGCAGGTGTGGAGT 3480
Db 3421 ACACCGCGTCGAGCTCGCGGCGCACGATGACGAACTGGTGTGCGCAGCAGGTGTGGAGT 3480
QY 3481 ACGGAAGCGACCCCTATCGGCGAGCCGATTCACCTTTCACGTTCTACGAGCTTTGCCAGG 3540
Db 3481 ACGGAAGCGACCCCTATCGGCGAGCCGATTCACCTTTCACGTTCTACGAGCTTTGCCAGG 3540
QY 3541 ACCTGGCTGGTCGATCAATGGCGGTATTACAGAGGCGGAGGATGCTCTGCGGCC 3600
Db 3541 ACCTGGCTGGTCGATCAATGGCGGTATTACAGAGGCGGAGGATGCTCTGCGGCC 3600
QY 3601 TACAGGCGACGGGATGGGCTTCACGTCGACCGCGTTGGGCACCTGGAATCGGTGTGCG 3660
Db 3601 TACAGGCGACGGGATGGGCTTCACGTCGACCGCGTTGGGCACCTGGAATCGGTGTGCG 3660
QY 3661 TGCTGACCCGCTCCGCGTCTCTGACCCGTGGCAAGAAAAAGTCCCGTTGCCAGTCTCTGA 3720
Db 3661 TGCTGACCCGCTCCGCGTCTCTGACCCGTGGCAAGAAAAAGTCCCGTTGCCAGTCTCTGA 3720
QY 3721 TCGACGAGGAATCGTCTGCTGTTGCTGCGCACCACTACAGAAATTCATATGGGAGA 3780
Db 3721 TCGACGAGGAATCGTCTGCTGTTGCTGCGCACCACTACAGAAATTCATATGGGAGA 3780
QY 3781 AGTACCCCAAGCTGTGCCCGACGCGCCGAGGATGTTTCGACTATTTTCAGCTCGCACCGGG 3840
Db 3781 AGTACCCCAAGCTGTGCCCGACGCGCCGAGGATGTTTCGACTATTTTCAGCTCGCACCGGG 3840
QY 3841 AGCGGTACCCGCTCAAGCTGGAACCTTCCGCTCATGTGCGGATCGGATTCACCCCGCG 3900
Db 3841 AGCGGTACCCGCTCAAGCTGGAACCTTCCGCTCATGTGCGGATCGGATTCACCCCGCG 3900
QY 3901 TGAAGAGTGGCGGACAGGTGGCGAAGCCTCGGAAGGTTGCGAGGAGCGGCGCTGG 3960
Db 3901 TGAAGAGTGGCGGACAGGTGGCGAAGCCTCGGAAGGTTGCGAGGAGCGGCGCTGG 3960
QY 3961 TGAACAACCGCTGGGTCAATGATGACCTGTGTGATTCGAAACGCTAGGGCTTTGTGGGT 4020
Db 3961 TGAACAACCGCTGGGTCAATGATGACCTGTGTGATTCGAAACGCTAGGGCTTTGTGGGT 4020
QY 4021 CAGTTCCGGCTGGGGTTTACAGCAGCAGCGCTTTACTGGCATTTCTAGGTTGACGCTT 4080
Db 4021 CAGTTCCGGCTGGGGTTTACAGCAGCAGCGCTTTACTGGCATTTCTAGGTTGACGCTT 4080
QY 4081 CTGATGGGCTGCCTGATTCGAGTGGTATTTGTCGCGAGCTGCCGTCGGGGAGCTGTT 4140
Db 4081 CTGATGGGCTGCCTGATTCGAGTGGTATTTGTCGCGAGCTGCCGTCGGGGAGCTGTT 4140
QY 4141 GGCTGGCTGGTGCGAGGATATATTGTGGTGTAAACAAATTCAGCCTTAGACAACTTAATA 4200
Db 4141 GGCTGGCTGGTGCGAGGATATATTGTGGTGTAAACAAATTCAGCCTTAGACAACTTAATA 4200
QY 4201 ACACATTCGCGACGTTTTTAATGTAATCTGGGCTATCCCCGGGGGATATCATAGGCCCG 4260
Db 4201 ACACATTCGCGACGTTTTTAATGTAATCTGGGCTATCCCCGGGGGATATCATAGGCCCG 4260
QY 4261 ATCTAGTAACATATGACCGCGGATATTTATCTAGTTTGGCGCTATATTTTG 4320
Db 4261 ATCTAGTAACATATGACCGCGGATATTTATCTAGTTTGGCGCTATATTTTG 4320
QY 4321 TTTTCTATCGGTATTAATGTAATTTGCGGACTCTAATCATAAAAACCACTCTCAT 4380
Db 4321 TTTTCTATCGGTATTAATGTAATTTGCGGACTCTAATCATAAAAACCACTCTCAT 4380
QY 4381 AATAACGTATGCAATTCATGTTAATTTATTAATGCTTTAAGTAAATTCACAGAAATAT 4440
Db 4381 AATAACGTATGCAATTCATGTTAATTTATTAATGCTTTAAGTAAATTCACAGAAATAT 4440
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QY 4441 ATGATAATCATCGCAAGACCGCAACAGGATTCATCTTTAAGAACTTTATTGCCAAATG 4500
Db 4441 ATGATAATCATCGCAAGACCGCAACAGGATTCATCTTTAAGAACTTTATTGCCAAATG 4500
QY 4501 TTTGAACGATCGTTCGTCGAGCTATGGGCCCA 4533
Db 4501 TTTGAACGATCGTTCGTCGAGCTATGGGCCCA 4533

RESULT 12
US-09-845-064-13
; Sequence 13, Application US/09845064
; Publication No. US20030175976A1
; GENERAL INFORMATION:
; APPLICANT: MERISTEM THERAPEUTICS
; TITLE OF INVENTION: CLEAN SYNTHETIC VECTORS, PLASMIDS, TRANSGENIC PLANTS
; TITLE OF INVENTION: AND PLANT PARTS CONTAINING SAID VECTORS, AND THEIR
; FILE REFERENCE: SynVec1
; CURRENT APPLICATION NUMBER: US/09/845,064
; CURRENT FILING DATE: 2001-04-27
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 6865
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Plasmid
; OTHER INFORMATION: pMRT1195
; FEATURE:
; NAME/KEY: rep origin
; LOCATION: (1)..(654)
; OTHER INFORMATION: Origin of replication ori RK2
; FEATURE:
; NAME/KEY: rep origin
; LOCATION: (655)..(1263)
; OTHER INFORMATION: Origin of replication ori Colei
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1264)..(2603)
; OTHER INFORMATION: NPT III gene coding for neomycin
; OTHER INFORMATION: phosphotransferase and kanamycin resistance
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2604)..(4098)
; OTHER INFORMATION: TrfA locus from RK2 coding for two proteins, P285
; OTHER INFORMATION: and P382, enabling the increase in the replication
; OTHER INFORMATION: rate
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4106)..(4271)
; OTHER INFORMATION: T-DNA left border
; FEATURE:
; NAME/KEY: terminator
; LOCATION: (4272)..(4559)
; OTHER INFORMATION: No. US20030175976Ala1line synthetase terminator
; FEATURE:
; NAME/KEY: gene
; LOCATION: (4575)..(5150)
; OTHER INFORMATION: Bar gene coding for phosphinotricin
; OTHER INFORMATION: acetyltransferase and glufosinate resistance
; FEATURE:
; NAME/KEY: intron
; LOCATION: (5174)..(5685)
; OTHER INFORMATION: Rice Actin Intron
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (5686)..(6626)
; OTHER INFORMATION: Rice Actin promoter
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (6626)..(6685)
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OTHER INFORMATION: MCS multiple cloning site

FEATURE:

NAME/KEY: misc feature

LOCATION: (6685)..(6858)

OTHER INFORMATION: r-DNA right border

US-09-845-064-13

Query Match 94.3%; Score 4531.4; DB 10; Length 6865;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 4532; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	CCGGCTGGTTCCTCGCGCTGGCTGGGCTGGGCGGCTATGGCCCTGCAAAACGGCCAG	60
Db	1	CCGGCTGGTTCCTCGCGCTGGCTGGGCTGGGCGGCTATGGCCCTGCAAAACGGCCAG	60
Qy	61	AAACCGCTCGAAGCGGTGTGCAGACACACCGCGCGCGGTGGGATACCTCGCGG	120
Db	61	AAACCGCGTGAAGCCGTGTGCAGACACACCGCGCGCGGTGGGATACCTCGCGG	120
Qy	121	AAACCTTGGCCCTCACTGACAGATGAGGGCGGACGTTGACACTTGAGGGCGCGACTCAC	180
Db	121	AAACCTTGGCCCTCACTGACAGATGAGGGCGGACGTTGACACTTGAGGGCGCGACTCAC	180
Qy	181	CCGGCGCGGCTTGACAGATGAGGGCGAGGCTCGATTTCGGCCGGCGACGTGGCTGGC	240
Db	181	CCGGCGCGGCTTGACAGATGAGGGCGAGGCTCGATTTCGGCCGGCGACGTGGCTGGC	240
Qy	241	CAGCTCGCAAAATCGCGGAAACGCTGATTTACGCGAGTTTCCCAACAGATGATGGA	300
Db	241	CAGCTCGCAAAATCGCGGAAACGCTGATTTACGCGAGTTTCCCAACAGATGATGGA	300
Qy	301	CAAGCTTGGGATGAAGTGCCTCGGTATTGACACTTGAGGGCGCGACTACTGACAGAT	360
Db	301	CAAGCTTGGGATGAAGTGCCTCGGTATTGACACTTGAGGGCGCGACTACTGACAGAT	360
Qy	361	GAGGGCGGATCTTGAACACTTTGAGGGCAGAGTGTGAAGATGAGGGCGCGACTAT	420
Db	361	GAGGGCGGATCTTGAACACTTTGAGGGCAGAGTGTGAAGATGAGGGCGCGACTAT	420
Qy	421	TGACATTTGAGGGCTGTCCACAGGCAAAATCCAGCATTTGCAAGGGTTTCGGCCGT	480
Db	421	TGACATTTGAGGGCTGTCCACAGGCAAAATCCAGCATTTGCAAGGGTTTCGGCCGT	480
Qy	481	TTTTTCGCCACCGCTAACCTGTCTTTAACTGCTTTAAACCAATATTTATAAACCCTG	540
Db	481	TTTTTCGCCACCGCTAACCTGTCTTTAACTGCTTTAAACCAATATTTATAAACCCTG	540
Qy	541	TTTTTAAACAGGGTGGCCCTGTGCGGTGAACGGCGACCGCGAGGGGGTGCCCCC	600
Db	541	TTTTTAAACAGGGTGGCCCTGTGCGGTGAACGGCGACCGCGAGGGGGTGCCCCC	600
Qy	601	CTTCTCGAACCCCTCCCGAAGGTATCGGTGTGAATACCGCACAGATCGTAAGAGA	660
Db	601	CTTCTCGAACCCCTCCCGAAGGTATCGGTGTGAATACCGCACAGATCGTAAGAGA	660
Qy	661	AAATACCGCATCAGGCGCTCTTCGGCTTCCTCGCTCACTGCTGCGCTCGGCTGTT	720
Db	661	AAATACCGCATCAGGCGCTCTTCGGCTTCCTCGCTCACTGCTGCGCTCGGCTGTT	720
Qy	721	CGGCTCGGCGAGCGGTATCAGCTCACTCAAGCGGTATACGGTTTATCCACAGATCA	780
Db	721	CGGCTCGGCGAGCGGTATCAGCTCACTCAAGCGGTATACGGTTTATCCACAGATCA	780
Qy	781	GGGATTAACCCAGGAAGATCATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAAACCGTAA	840
Db	781	GGGATTAACCCAGGAAGATCATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAAACCGTAA	840
Qy	841	AAGCCCGCTGTGCTGGCGTTTTCATAGGCTCCGCCCTGACGAGCATCAAAAAT	900
Db	841	AAGCCCGCTGTGCTGGCGTTTTCATAGGCTCCGCCCTGACGAGCATCAAAAAT	900
Qy	901	CGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAGATACCAAGGGTTTCCC	960
Db	901	CGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAGATACCAAGGGTTTCCC	960

Db	901	CGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAAGGGTTTCCC	960
Qy	961	CCTGGAAGCTCCCTCGTGGCGCTCTCTGTTCCGACCTCGCGCTTACCGGATACCTCTCC	1020
Db	961	CCTGGAAGCTCCCTCGTGGCGCTCTCTGTTCCGACCTCGCGCTTACCGGATACCTCTCC	1020
Qy	1021	GCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGT	1080
Db	1021	GCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGT	1080
Qy	1081	TCCGTGTAGTCTGTTCCGCTCCAAGCTGGGCTGTGTCGCAAAACCCCGCTTCAGCCCGAC	1140
Db	1081	TCCGTGTAGTCTGTTCCGCTCCAAGCTGGGCTGTGTCGCAAAACCCCGCTTCAGCCCGAC	1140
Qy	1141	CGCTGCGCTTATCCGCTAACCTATCTCTTGGTCAACCCGCTAAGACACGACTTATCG	1200
Db	1141	CGCTGCGCTTATCCGCTAACCTATCTCTTGGTCAACCCGCTAAGACACGACTTATCG	1200
Qy	1201	CCACTGGCAGCAGCTTCTACCAATAATCCGCGATAAACCCAGCGAAACCATTTGAGGTGAT	1260
Db	1201	CCACTGGCAGCAGCTTCTACCAATAATCCGCGATAAACCCAGCGAAACCATTTGAGGTGAT	1260
Qy	1261	AGTAAAGATTATCCGAGGTATGAAAACGAGAAATTGACCTTTACAGAAATCTCTATGA	1320
Db	1261	AGTAAAGATTATCCGAGGTATGAAAACGAGAAATTGACCTTTACAGAAATCTCTATGA	1320
Qy	1321	AGCGCCATATTTAAAAGCTTACCAAGCAAGAGGATGAAGAGATGAGGAGGAGGATG	1380
Db	1321	AGCGCCATATTTAAAAGCTTACCAAGCAAGAGGATGAAGAGATGAGGAGGAGGATG	1380
Qy	1381	CCTTGAATATATTGACAATCTGATAAGATAATACATCTTTTATATAGAAATATCGCCG	1440
Db	1381	CCTTGAATATATTGACAATCTGATAAGATAATACATCTTTTATATAGAAATATCGCCG	1440
Qy	1441	TATGTAAGATTTCAGGGGCAAGGCATAGGCGCGCTTATCAATATATCTATAGAAAT	1500
Db	1441	TATGTAAGATTTCAGGGGCAAGGCATAGGCGCGCTTATCAATATATCTATAGAAAT	1500
Qy	1501	GGCAAGCATAAAACTTGCATGGACTAATGCTTGAACCCAGGACAATAACCTATAG	1560
Db	1501	GGCAAGCATAAAACTTGCATGGACTAATGCTTGAACCCAGGACAATAACCTATAG	1560
Qy	1561	CTTGTAAATTTACCAAAATTTGGTTTCAAAATCGGCTCGCTCGATCTATGTTACG	1620
Db	1561	CTTGTAAATTTACCAAAATTTGGTTTCAAAATCGGCTCGCTCGATCTATGTTACG	1620
Qy	1621	CMACTTTGAAAACAACTTTGAAAAAGCTGTTTCTGTTTAAAGTTTTAGAAATGCAA	1680
Db	1621	CMACTTTGAAAACAACTTTGAAAAAGCTGTTTCTGTTTAAAGTTTTAGAAATGCAA	1680
Qy	1681	GGACAGTGAATTTGGAGTTCTGTTTATATTTAGCTTCTTGGGGTATCTTTAAATACT	1740
Db	1681	GGACAGTGAATTTGGAGTTCTGTTTATATTTAGCTTCTTGGGGTATCTTTAAATACT	1740
Qy	1741	GTAGAAAAGAGGAAGAAATAAATGCTTAAATGAGAAATACACCGAAATGAAAAA	1800
Db	1741	GTAGAAAAGAGGAAGAAATAAATGCTTAAATGAGAAATACACCGAAATGAAAAA	1800
Qy	1801	ACTGATCGAAAAATACCGCTGCGTAAAAATACGGAAGGAAATGCTCTGCTAAGGTATA	1860
Db	1801	ACTGATCGAAAAATACCGCTGCGTAAAAATACGGAAGGAAATGCTCTGCTAAGGTATA	1860
Qy	1861	TAACTGGTGGGAGAAATGAAAAACCTATATTTAAAAATGACGGAAGCGGTATAAAG	1920
Db	1861	TAACTGGTGGGAGAAATGAAAAACCTATATTTAAAAATGACGGAAGCGGTATAAAG	1920
Qy	1921	GACCACTATGATGTGAAACGGGAAAGGACATGATGCTTATGCTGCTGAAAGAAAGCTGCC	1980
Db	1921	GACCACTATGATGTGAAACGGGAAAGGACATGATGCTTATGCTGCTGAAAGAAAGCTGCC	1980
Qy	1981	TGTTCCAAAGGCTCTGCACTTTGAAACGGCATGATGCTGGAGCAATCTGCTCATGATGA	2040
Db	1981	TGTTCCAAAGGCTCTGCACTTTGAAACGGCATGATGCTGGAGCAATCTGCTCATGATGA	2040

Qy	2041	GGCCGATGGCGTCTTTGCTCGGAAGAGTATGAAGATGAACAAGCCCTGAAAAGATTAT	2100
Db	2041	GGCCGATGGCGTCTTTGCTCGGAAGAGTATGAAGATGAACAAGCCCTGAAAAGATTAT	2100
Qy	2101	CGAGCTGTATGCGGAGTGCATCAGGCTCTTTCACTCCATCGACATATCGGATTGTCCTTA	2160
Db	2101	CGAGCTGTATGCGGAGTGCATCAGGCTCTTTCACTCCATCGACATATCGGATTGTCCTTA	2160
Qy	2161	TACGAATAGCTTAGACAGCCGCTTAGCCGAATTGGATTACTTGAATTAACGATCTGGC	2220
Db	2161	TACGAATAGCTTAGACAGCCGCTTAGCCGAATTGGATTACTTGAATTAACGATCTGGC	2220
Qy	2221	CGATGTGGATTGGGAACCTGGGAAGAGACACTCCATTTAAAGATCCGCGGAGCTGTA	2280
Db	2221	CGATGTGGATTGGGAACCTGGGAAGAGACACTCCATTTAAAGATCCGCGGAGCTGTA	2280
Qy	2281	TGATTTTTTAAAGACGGAAAGCCGGAAGGAACTTGTCTTTTCCACGGCGACCTGGG	2340
Db	2281	TGATTTTTTAAAGACGGAAAGCCGGAAGGAACTTGTCTTTTCCACGGCGACCTGGG	2340
Qy	2341	AGACAGCAACATCTTTCTGAAAAGATGGCAAAGTAAAGTGGCTTTATTGATCTTGGGGAAG	2400
Db	2341	AGACAGCAACATCTTTCTGAAAAGATGGCAAAGTAAAGTGGCTTTATTGATCTTGGGGAAG	2400
Qy	2401	CGGACGGCGGACAAAGTGGTATGACATTTGCCTTCTGCGTCCGCTCGATCAGGGAGGATAT	2460
Db	2401	CGGACGGCGGACAAAGTGGTATGACATTTGCCTTCTGCGTCCGCTCGATCAGGGAGGATAT	2460
Qy	2461	CGGGGAAGAACAGTATGTCAGACTATTTTTTGACTTACTGGGGATCAAGCTGATTGGGA	2520
Db	2461	CGGGGAAGAACAGTATGTCAGACTATTTTTTGACTTACTGGGGATCAAGCTGATTGGGA	2520
Qy	2521	GAAAAATAAATATATATTTTACTGGATGAATTTGTTTATGTAACCTAGATGTGGCGCAACG	2580
Db	2521	GAAAAATAAATATATATTTTACTGGATGAATTTGTTTATGTAACCTAGATGTGGCGCAACG	2580
Qy	2581	ATCCCGGACACAGCAGGCGCACACTCTTCCGCATCAAGTGTTTTGGCTCTCAGG	2640
Db	2581	ATCCCGGCGACAGCAGGAGCGCACCCACTTCTCCGCATCAAGTGTTTTGGCTCTCAGG	2640
Qy	2641	CCGAGGCCACCGCAAGTATTTGGGCAAGGGTCCGCTGGTATTCGTGACAGGGCAAGATTC	2700
Db	2641	CCGAGGCCACCGCAAGTATTTGGGCAAGGGTCCGCTGGTATTCGTGACAGGGCAAGATTC	2700
Qy	2701	GGAATACCAAGTACGAGAAGACGGCCAGACGGTCTACGGGACCGACTTCATTGCCGATA	2760
Db	2701	GGAATACCAAGTACGAGAAGACGGCCAGACGGTCTACGGGACCGACTTCATTGCCGATA	2760
Qy	2761	AGGTGGATTATCTGGACACCAAGGCACCGCGGGTCAAAATCAGGAATAAGGGCACATTG	2820
Db	2761	AGGTGGATTATCTGGACACCAAGGCACCGCGGGTCAAAATCAGGAATAAGGGCACATTG	2820
Qy	2821	CCCCGGCTGAGTCGGGGCAATCCCGCAAGAGGGTGAATGAATCGGACGCTTTGACCCGGA	2880
Db	2821	CCCCGGCTGAGTCGGGGCAATCCCGCAAGAGGGTGAATGAATCGGACGCTTTGACCCGGA	2880
Qy	2881	AGGCATACAGGAAGAACTGATCGACGCGGGTTTTCCGCGGAGGATCGCCAAACCATCG	2940
Db	2881	AGGCATACAGGAAGAACTGATCGACGCGGGTTTTCCGCGGAGGATCGCCAAACCATCG	2940
Qy	2941	CNAGCCGACCGTCAATCGGTGCGCCCGCGGAAACCTTCCAGTCCGCTCGATGGTCC	3000
Db	2941	CNAGCCGACCGTCAATCGGTGCGCCCGCGGAAACCTTCCAGTCCGCTCGATGGTCC	3000
Qy	3001	AGCAAGCTACGGCCCAAGATCGAGCGCACAGCTGCAACTGGCTCCCCCTGCCCTGCCCG	3060
Db	3001	AGCAAGCTACGGCCCAAGATCGAGCGCACAGCTGCAACTGGCTCCCCCTGCCCTGCCCG	3060
Qy	3061	CGCCATCGGCGCGCTGGAGGCTTCGGCTGCTCGAAACAGGAGGCGGAGGTTTGGCGA	3120
Db	3061	CGCCATCGGCGCGCTGGAGGCTTCGGCTGCTCGAAACAGGAGGCGGAGGTTTGGCGA	3120

Qy	3121	AGTCGATGACCATCGACACGCGAGGAACTATGACGACCAAGAGCGAAAAACCCGCGCG	3180
Db	3121	AGTCGATGACCATCGACACGCGAGGAACTATGACGACCAAGAGCGAAAAACCCGCGCG	3180
Qy	3181	AGGACCTGGCAAAAACAGGTCAGGAGGCCAAGAGGCCCGCTTGTGTAACACACCAAGC	3240
Db	3181	AGGACCTGGCAAAAACAGGTCAGGAGGCCAAGAGGCCCGCTTGTGTAACACACCAAGC	3240
Qy	3241	AGCAGATCAAGGAAATGACAGCTTTCCTGTTTCGATATTGCGCGTGGCGGACACCATGC	3300
Db	3241	AGCAGATCAAGGAAATGACAGCTTTCCTGTTTCGATATTGCGCGTGGCGGACACCATGC	3300
Qy	3301	GAGCGATGCCAAAACGACACGGCCGCTCTGCCCCCTGTTTCAACCGCGCAACAAGAAATCC	3360
Db	3301	GAGCGATGCCAAAACGACACGGCCGCTCTGCCCCCTGTTTCAACCGCGCAACAAGAAATCC	3360
Qy	3361	CGCGCAGGCGCTGCAAAAACAAAGGTCATTTTCCAGCTCAACAAAGGACGTAAGATCACCT	3420
Db	3361	CGCGCAGGCGCTGCAAAAACAAAGGTCATTTTCCAGCTCAACAAAGGACGTAAGATCACCT	3420
Qy	3421	ACACCGCGCTCGAGCTGCGGGCCGACGATGACGAACTGGTGGCAGCAGGTTGAGAT	3480
Db	3421	ACACCGCGCTCGAGCTGCGGGCCGACGATGACGAACTGGTGGCAGCAGGTTGAGAT	3480
Qy	3481	ACGCGAAGCGCACCCCTATCGCGAGCCGATCACCTTTCACGTTTCTACGAGCTTTGCCAGG	3540
Db	3481	ACGCGAAGCGCACCCCTATCGCGAGCCGATCACCTTTCACGTTTCTACGAGCTTTGCCAGG	3540
Qy	3541	ACCTGGCTGGTGCATCAATTGGCCGATATTAACGAAAGCCGAGGAATGCTGTGCGGCC	3600
Db	3541	ACCTGGCTGGTGCATCAATTGGCCGATATTAACGAAAGCCGAGGAATGCTGTGCGGCC	3600
Qy	3601	TACAGCGCAGCGGATGGGCTTACGTCGCGCGCTGGCAACCTGGAACTCGGTGTCG	3660
Db	3601	TACAGCGCAGCGGATGGGCTTACGTCGCGCGCTGGCAACCTGGAACTCGGTGTCG	3660
Qy	3661	TGCTGCACCGCTTCCGCGCTCGTGACCGCTGGCAAGAAACGTCGCCGTGTCAGGCTCTGA	3720
Db	3661	TGCTGCACCGCTTCCGCGCTCGTGACCGCTGGCAAGAAACGTCGCCGTGTCAGGCTCTGA	3720
Qy	3721	TGCAACGAGGAAATCGTGTGCTGTTTGTGGCGACCACTACAGGAAATTCATATGGGAGA	3780
Db	3721	TGCAACGAGGAAATCGTGTGCTGTTTGTGGCGACCACTACAGGAAATTCATATGGGAGA	3780
Qy	3781	AGTACCGCAGCTGTCGCGACGGCCGCGGATGTTCCGACTATTTTCAGCTCCGACCGGG	3840
Db	3781	AGTACCGCAGCTGTCGCGACGGCCGCGGATGTTCCGACTATTTTCAGCTCCGACCGGG	3840
Qy	3841	AGCCGTACCCGCTCAAAGCTGGAAACCTTCCGCTCATGTGCGGATCGGATTCACCCGCG	3900
Db	3841	AGCCGTACCCGCTCAAAGCTGGAAACCTTCCGCTCATGTGCGGATCGGATTCACCCGCG	3900
Qy	3901	TGAAGAAGTGGCGCAGCAGGTCGGCGAAGCCTGTCGGAAGAGTTGCGAGGCGGCGCTGG	3960
Db	3901	TGAAGAAGTGGCGCAGCAGGTCGGCGAAGCCTGTCGGAAGAGTTGCGAGGCGGCGCTGG	3960
Qy	3961	TGGAAACACGCTCGGCTCAATGATGACCTGGTGAATTCGAAACCTAGGGCTTTGCGGGT	4020
Db	3961	TGGAAACACGCTCGGCTCAATGATGACCTGGTGAATTCGAAACCTAGGGCTTTGCGGGT	4020
Qy	4021	CAGTTCGGCTGGGGTTTCCAGCAGCAGCGCTTTTACTGGCATTTCTAGGTTCAGCTCTT	4080
Db	4021	CAGTTCGGCTGGGGTTTCCAGCAGCAGCGCTTTTACTGGCATTTCTAGGTTCAGCTCTT	4080
Qy	4081	CTCATGGGCTGCTGATTCAGTGGTGAATTTGTGCGGAGCTGCCGTCGGGAGCTGTT	4140
Db	4081	CTCATGGGCTGCTGATTCAGTGGTGAATTTGTGCGGAGCTGCCGTCGGGAGCTGTT	4140
Qy	4141	GGCTGCTGTCGACGATATATTGGTGTAAACAAATTTAGCCTTAGACAACCTTAATA	4200
Db	4141	GGCTGCTGTCGACGATATATTGGTGTAAACAAATTTAGCCTTAGACAACCTTAATA	4200
Qy	4201	ACACATTTGCGGACGTTTTTAAATGACTAGGGGCTATCCCCCGGGGATATCCATAGGCCCG	4260

[illegible]

RESULT 13

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US-09-845-064-17
; Sequence 17, Application US/09845064
; Publication No. US20030175976A1
; GENERAL INFORMATION:
; APPLICANT: MERISTEM THERAPEUTICS
; TITLE OF INVENTION: CLEAN SYNTHETIC VECTORS, PLASMIDS, TRANSGENIC PLANTS
; TITLE OF INVENTION: AND PLANT PARTS CONTAINING SAID VECTORS, AND THEIR
; TITLE OF INVENTION: METHODS OF PRODUCTION
; FILE REFERENCE: SynVec1
; CURRENT APPLICATION NUMBER: US/09/845,064
; CURRENT FILING DATE: 2001-04-27
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 7503
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Plasmid
; OTHER INFORMATION: pMT1203
; FEATURE:
; NAME/KEY: rep_origin
; LOCATION: (1)..(654)
; OTHER INFORMATION: Origin of replication ori RK2
; FEATURE:
; NAME/KEY: rep_origin
; LOCATION: (655)..(1263)
; OTHER INFORMATION: Origin of replication ori ColeI
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1264)..(2603)
; OTHER INFORMATION: NPT III gene coding for neomycin
; OTHER INFORMATION: phosphotransferase and kanamycin resistance
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2604)..(4098)
; OTHER INFORMATION: TrfA locus from RK2 coding for two proteins, p285
; OTHER INFORMATION: and p382; enabling the increase in the rate of
; OTHER INFORMATION: replication
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4106)..(4271)
; OTHER INFORMATION: T-DNA left border
; FEATURE:
; NAME/KEY: terminator
; LOCATION: (4272)..(4559)
; OTHER INFORMATION: No. US20030175976A1alaine synthetase terminator
; FEATURE:

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Qy	601	CTTCTCGAACCCCTCCCGGAAAGGTATGCGGGTGTGAATACCGCACAGATCGGTAAAGAGA	660
Db	601	CTTCTCGAACCCCTCCCGGAAAGGTATGCGGGTGTGAATACCGCACAGATCGGTAAAGAGA	660
Qy	661	AAATACCGCATCAGGCGCTCTTCGGCTTCCTCGCTCACTGACTCGTGGCTCGGTGCTT	720
Db	661	AAATACCGCATCAGGCGCTCTTCGGCTTCCTCGCTCACTGACTCGTGGCTCGGTGCTT	720
Qy	721	CGGCTCGGCGAGGGGTATCAGTCACTCAAAGGCGGTAAATAGCGTTATCCACAGAATCA	780
Db	721	CGGCTCGGCGAGGGGTATCAGTCACTCAAAGGCGGTAAATAGCGTTATCCACAGAATCA	780
Qy	781	GGGGATAACCGAGGAAGACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAA	840
Db	781	GGGGATAACCGAGGAAGACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAA	840
Qy	841	AAGGCCCGCTTGTGGCGTTTTCATAGGCTCGCCCCCTCGACGAGCATCAAAAAAT	900
Db	841	AAGGCCCGCTTGTGGCGTTTTCATAGGCTCGCCCCCTCGACGAGCATCAAAAAAT	900
Qy	901	CGAGCTCAAGTCAAGAGGTGGCGAAACCCGACAGGACTATAAGATACACAGGCGTTTCCC	960
Db	901	CGAGCTCAAGTCAAGAGGTGGCGAAACCCGACAGGACTATAAGATACACAGGCGTTTCCC	960
Qy	961	CCTTGAAGCTCCCTGTCGCTCTCCTGTTCCGACCTGCGCTTACCGGATACCTGTCC	1020
Db	961	CCTTGAAGCTCCCTGTCGCTCTCCTGTTCCGACCTGCGCTTACCGGATACCTGTCC	1020
Qy	1021	GCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCATAGCTCAGCGCTGAGGTATCTCAGT	1080
Db	1021	GCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCATAGCTCAGCGCTGAGGTATCTCAGT	1080
Qy	1081	TCGGTGTAGTTCGTTTCGCTCAAGCTGGGCTGTGTGCACGAAACCCCGCTTACGCCGAC	1140
Db	1081	TCGGTGTAGTTCGTTTCGCTCAAGCTGGGCTGTGTGCACGAAACCCCGCTTACGCCGAC	1140
Qy	1141	CGCTGCGCCTTATCCCGTAACTACTGCTTTCGAGTCCAAACCCGGTAAACACGACTTATCG	1200
Db	1141	CGCTGCGCCTTATCCCGTAACTACTGCTTTCGAGTCCAAACCCGGTAAACACGACTTATCG	1200
Qy	1201	CCACTGGCAGCAGCTTCTACCAATAATCCGCGATAAACCCAGCGAAACCATTCAGGTGAT	1260
Db	1201	CCACTGGCAGCAGCTTCTACCAATAATCCGCGATAAACCCAGCGAAACCATTCAGGTGAT	1260
Qy	1261	AGGTAAAGTATACCGAGGTATGAAAACGAGAAATGGACCTTTACAGAAATCTCTATGA	1320
Db	1261	AGGTAAAGTATACCGAGGTATGAAAACGAGAAATGGACCTTTACAGAAATCTCTATGA	1320
Qy	1321	AGCGCCATATTTAAAGAGCTTACCAAGCAGAGAGGATGAGAGGATCAGGAGCGCAGATTG	1380
Db	1321	AGCGCCATATTTAAAGAGCTTACCAAGCAGAGAGGATGAGAGGATCAGGAGCGCAGATTG	1380
Qy	1381	CTTTGAATATATTGACAAATCTGATAAGATAAATACATCTTTTATATAGAAGATATCCCGG	1440
Db	1381	CTTTGAATATATTGACAAATCTGATAAGATAAATACATCTTTTATATAGAAGATATCCCGG	1440
Qy	1441	TATGTAAGGATTTTCAGGGGCAAGGCATAGCAGCGCGCTTATCAATATATCTATAGAAT	1500
Db	1441	TATGTAAGGATTTTCAGGGGCAAGGCATAGCAGCGCGCTTATCAATATATCTATAGAAT	1500
Qy	1501	GGGCAAGCATAAAAACTTGATCGACTAATGCTTTGAAACCCAGGACATAACCTTATAG	1560
Db	1501	GGGCAAGCATAAAAACTTGATCGACTAATGCTTTGAAACCCAGGACATAACCTTATAG	1560
Qy	1561	CTTCTAAATCTTACCAAAATTTGGTTTCAAATTCGGCTCGCTCGATCTATGTTATACG	1620
Db	1561	CTTCTAAATCTTACCAAAATTTGGTTTCAAATTCGGCTCGCTCGATCTATGTTATACG	1620
Qy	1621	CCAACTTTGAAAAACAACCTTTGAAAAAGCTGTTTTCTGGTATTTTAAGGTTTTAGAAATCAA	1680
Db	1621	CCAACTTTGAAAAACAACCTTTGAAAAAGCTGTTTTCTGGTATTTTAAGGTTTTAGAAATCAA	1680

Qy	1681	GGAAACAGTGAATTTGGAGTTTCGTCTTGTTATAATTAGCTTCTTCGGGTTACTTTTAAATACT	1741
Db	1681	GGAAACAGTGAATTTGGAGTTTCGTCTTGTTATAATTAGCTTCTTCGGGTTACTTTTAAATACT	1740
Qy	1741	GTAGAAAAGAGGAAGGARATATAAATGCTTAAATGAGAAATGAGAAATACACCGGAAATTGAAAA	1800
Db	1741	GTAGAAAAGAGGAAGGAATAATAATGCTTAAATGAGAAATGAGAAATACACCGGAAATTGAAAA	1800
Qy	1801	ACTGATCGAAAAATACCGCTTCGCTTAAAGATACGGAAGGAATCTCTCTGCTAAGGTATA	1860
Db	1801	ACTGATCGAAAAATACCGCTTCGCTTAAAGATACGGAAGGAATCTCTCTGCTAAGGTATA	1860
Qy	1861	TAAGCTGGTGGGAGAAAAATGAAAAACCTATATTATTTAAAAATGACGACAGCCGGTATAAAG	1920
Db	1861	TAAGCTGGTGGGAGAAAAATGAAAAACCTATATTATTTAAAAATGACGACAGCCGGTATAAAG	1920
Qy	1921	GACCACTATGATGTGAACGGGAAAAAGNACATGATGCTATGCTCGAAGGAAGCTGCC	1980
Db	1921	GACCACTATGATGTGAACGGGAAAAAGNACATGATGCTATGCTCGAAGGAAGCTGCC	1980
Qy	1981	TGTTCCAAAGGTCCTGTCACCTTTTCAAACGGCATGATGCTGGAGCAATCTGCTCATAGTGA	2040
Db	1981	TGTTCCAAAGGTCCTGTCACCTTTGCAACGGCATGATGCTGGAGCAATCTGCTCATAGTGA	2040
Qy	2041	GGCCGATGGCGTCTTTGCTCGGAAGAGTATGAAGATGAACAAAGCCCTGAAAGATTAT	2100
Db	2041	GGCCGATGGCGTCTTTGCTCGGAAGAGTATGAAGATGAACAAAGCCCTGAAAGATTAT	2100
Qy	2101	CGAGCTGTATGCGGAGTGCAATCAGGCTCTTTCACTCCATCGACATATCGGATTTGCCCTA	2160
Db	2101	CGAGCTGTATGCGGAGTGCAATCAGGCTCTTTCACTCCATCGACATATCGGATTTGCCCTA	2160
Qy	2161	TACGAATAGCTTATAGACAGCCGCTTAGCCGAATTTGGATTACTTACTGAATAACGATCTGGC	2220
Db	2161	TACGAATAGCTTATAGACAGCCGCTTAGCCGAATTTGGATTACTTACTGAATAACGATCTGGC	2220
Qy	2221	CGATGTGGATTGCGAAAACTGGGAAGAGACATCCCATTTAAAGATCCGCGCGAGCTGTA	2280
Db	2221	CGATGTGGATTGCGAAAACTGGGAAGAGACATCCCATTTAAAGATCCGCGCGAGCTGTA	2280
Qy	2281	TGATTTTTTAAAGACGGAAGAAAGCCGAGAGGAACCTTGCTTTTCCACCGCGACCTGGG	2340
Db	2281	TGATTTTTTAAAGACGGAAGAAAGCCGAGAGGAACCTTGCTTTTCCACCGCGACCTGGG	2340
Qy	2341	AGACAGCAACATCTTTGTGAAAGATGCAAAAGTAAGTGGCTTTTATTGATCTTGGGAGAAG	2400
Db	2341	AGACAGCAACATCTTTGTGAAAGATGCAAAAGTAAGTGGCTTTTATTGATCTTGGGAGAAG	2400
Qy	2401	CGGACGGCGGACAAGTGGTATGACATTGCTCTTCGCTCCGTCGATACAGGAGGATAT	2460
Db	2401	CGGACGGCGGACAAGTGGTATGACATTGCTCTTCGCTCCGTCGATACAGGAGGATAT	2460
Qy	2461	CGGGGAAGAACAGTATGTCAGCTATTTTTTGTGACTTACTGGGATCAAGCCTGATTCGGA	2520
Db	2461	CGGGGAAGAACAGTATGTCAGCTATTTTTTGTGACTTACTGGGATCAAGCCTGATTCGGA	2520
Qy	2521	GAAATATAATTTATATTTTACTTGGATGAATTTTGTAGTACCTAGATGTGGCGCAACG	2580
Db	2521	GAAATATAATTTATATTTTACTTGGATGAATTTTGTAGTACCTAGATGTGGCGCAACG	2580
Qy	2581	ATGCGCGGCGACAGCAGGAGCGCACCGACTTCTTCCGCATCAAGTGTTCAGGTCACAG	2640
Db	2581	ATGCGCGGCGACAGCAGGAGCGCACCGACTTCTTCCGCATCAAGTGTTCAGGTCACAG	2640
Qy	2641	CCGAGGCCACCGCAAGTATTTTGGCAAGGGGTCTGTTATTCGTCGAGGGCAAGATTTC	2700
Db	2641	CCGAGGCCACCGCAAGTATTTTGGCAAGGGGTCTGTTATTCGTCGAGGGCAAGATTTC	2700
Qy	2701	GGATACCAAGTACGAGAAAGACGGCCAGACGGTCTACGGACCGACTTTCATTCGCCGATA	2760
Db	2701	GGATACCAAGTACGAGAAAGACGGCCAGACGGTCTACGGACCGACTTTCATTCGCCGATA	2760
Qy	2761	AGGTGGATTATCTTGGACACCAAGGACACGAGCGGGTCAAAATCAGGAATAAGGGCACATTG	2820



Db	2761		AGGTGGATTTATCTCGACACCAAGGCAACAGCGGGTCAAAATCAGGAATAAGGOCACATTG	2820
Qy	2821	CCCCGGCGTGAAGTCCGGGCAATCCGCAAGAGAGGTGAATGAATCGGACGTTTGACCGGA	2880	
Db	2821	CCCCGGCGTGAAGTCCGGGCAATCCGCAAGAGAGGTGAATGAATCGGACGTTTGACCGGA	2880	
Qy	2881	AGGCATACAGCGAAGAACTGANTGACGCGGGGTTTCCGCGAGGATGCGCGAACAATCG	2940	
Db	2881	AGGCATACAGCGAAGAACTGANTGACGCGGGGTTTCCGCGAGGATGCGCGAACAATCG	2940	
Qy	2941	CAAGCCACCGCTCATCGTCCGCGCGCGGAAACCTTCCAGTCCGTCGGCTCGATGGTCC	3000	
Db	2941	CAAGCCACCGCTCATCGTCCGCGCGCGGAAACCTTCCAGTCCGTCGGCTCGATGGTCC	3000	
Qy	3001	AGCAAGCTACGGCCAAAGATCAGCGCGCACAGCGTGCAACTGGTCCCGCTGCCCTGCCCG	3060	
Db	3001	AGCAAGCTACGGCCAAAGATCAGCGCGCACAGCGTGCAACTGGTCCCGCTGCCCTGCCCG	3060	
Qy	3061	CGCCATCGGCGCGCTGGAGGTTTCGCGTCTCGAAACAGGAGGCGCAGGTTTGCGGA	3120	
Db	3061	CGCCATCGGCGCGCTGGAGGTTTCGCGTCTCGAAACAGGAGGCGCAGGTTTGCGGA	3120	
Qy	3121	AGTCGATGACCATCGACACGCGAGGAACTATGACGACCAAGAACGNAAAACCGCGCGG	3180	
Db	3121	AGTCGATGACCATCGACACGCGAGGAACTATGACACCAAGAACGNAAAACCGCGCGG	3180	
Qy	3181	AGGACCTGGCAAAACAGGTCAGCGAGGCCAAGCAGGCGGCTTCTCGAAACACAGAAAGC	3240	
Db	3181	AGGACCTGGCAAAACAGGTCAGCGAGGCCAAGCAGGCGGCTTCTCGAAACACAGAAAGC	3240	
Qy	3241	AGCAGATCAAGGAAATCAGCTTTCTTGTTCGATATTGGCCGCTGGCGGACACGATGC	3300	
Db	3241	AGCAGATCAAGGAAATCAGCTTTCTTGTTCGATATTGGCCGCTGGCGGACACGATGC	3300	
Qy	3301	GAGCGATGCCAAGCACGCGCGCGCTCTGCGCTGTTCACACGCGCAACAAGAAATTC	3360	
Db	3301	GAGCGATGCCAAGCACGCGCGCGCTCTGCGCTGTTCACACGCGCAACAAGAAATTC	3360	
Qy	3361	CGCGGAGGCGCTGCAAAACAAGGTCAATTTTCAGCTCAACAAGGACGTCAAGATCACCT	3420	
Db	3361	CGCGGAGGCGCTGCAAAACAAGGTCAATTTTCAGCTCAACAAGGACGTCAAGATCACCT	3420	
Qy	3421	ACACCGCGCTCGAGCTCGGGCCGACGATGACGAACTGGTGTGGCAGAGCTGTGGAGT	3480	
Db	3421	ACACCGCGCTCGAGCTCGGGCCGACGATGACGAACTGGTGTGGCAGAGCTGTGGAGT	3480	
Qy	3481	ACGGGAAGCGCACCCCTATCGGAGCGGATCACTTTACGTTCTACGAGCTTTCGACAGG	3540	
Db	3481	ACGGGAAGCGCACCCCTATCGGAGCGGATCACTTTACGTTCTACGAGCTTTCGACAGG	3540	
Qy	3541	ACCTGGGCTCGTTCGATCAATGGCGGTTATACGAGGCGGAGGAAATCGCTCTCGCGC	3600	
Db	3541	ACCTGGGCTCGTTCGATCAATGGCGGTTATACGAGGCGGAGGAAATCGCTCTCGCGC	3600	
Qy	3601	TACAGGCGACGGCGATGGGCTTCACTGTCACGCGCGCTTGGGCACTCGGAATCGGTTCGC	3660	
Db	3601	TACAGGCGACGGCGATGGGCTTCACTGTCACGCGCGCTTGGGCACTCGGAATCGGTTCGC	3660	
Qy	3661	TGCTGCACCGCTTCGGGCTCCTGGACGCTGGCAAGAAACGTCCTCGGTTCGAGTCTCTGA	3720	
Db	3661	TGCTGCACCGCTTCGGGCTCCTGGACGCTGGCAAGAAACGTCCTCGGTTCGAGTCTCTGA	3720	
Qy	3721	TCGACGAGGAAATCGTCTGCTGCTTGTCTGGCGACCACTACAGAAATTCATATGGAGA	3780	
Db	3721	TCGACGAGGAAATCGTCTGCTGCTGCTTGTCTGGCGACCACTACAGAAATTCATATGGAGA	3780	
Qy	3781	AGTACCGCAAGCTGTCGCGACGCGCGAGGATGTTTCGACTATTTTCAGCTCGCACCGGG	3840	
Db	3781	AGTACCGCAAGCTGTCGCGACGCGCGAGGATGTTTCGACTATTTTCAGCTCGCACCGGG	3840	
Qy	3841	AGCCGTAACCGCTCAAGCTGGAACCTTCCGCTCATGTGCGGATCGGATTCACCCCGG	3900	

3941	AGCGGTACCGCTCAAGCTCGGAACCTTCGCGCTCATGTGCGGATCGGATTCACCGCGG	3900
3901	TGAAGAAGTGGCGGAGCAGCTCGGCGAAGCCCTCGAAGAGTTGCGAGGCGAGCGGCTCG	3960
3901	TGAAGAAGTGGCGGAGCAGCTCGGCGAAGCCCTCGAAGAGTTGCGAGGCGAGCGGCTCG	3960
3961	TGGAACAAGCTGGGTCAATGATGACCTGTGTGATTCGAAACGCTAGGGGCTTTGTGGGGT	4020
3961	TGGAACAAGCTGGGTCAATGATGACCTGTGTGATTCGAAACGCTAGGGGCTTTGTGGGGT	4020
4021	CAGTTCCGGCTGGGGTTACAGCAGCGCCTTTACTTGGCATTTCTAGGCATTTCTAGGTTGACGCTTT	4080
4021	CAGTTCCGGCTGGGGTTACAGCAGCGCCTTTACTTGGCATTTCTAGGCATTTCTAGGTTGACGCTTT	4080
4081	CTGATGGGCTGCCGTATCGAGTGGTGATTTTGTGCGGAGCTCCGGTCGGGAGCTGTT	4140
4081	CTGATGGGCTGCCGTATCGAGTGGTGATTTTGTGCGGAGCTCCGGTCGGGAGCTGTT	4140
4141	GGCTGGCTGGTGGCAGGATATATTGTGGTGTAAACAAATTGACGCTTAGACAACTTAAATA	4200
4141	GGCTGGCTGGTGGCAGGATATATTGTGGTGTAAACAAATTGACGCTTAGACAACTTAAATA	4200
4201	ACACATTTGGCGAGCTTTTAAATCTACTTGGGGCTATCCCGGGGGATATCCATAGGCCCG	4260
4201	ACACATTTGGCGAGCTTTTAAATCTACTTGGGGCTATCCCGGGGGATATCCATAGGCCCG	4260
4261	ATCTAGTAAACATAATGACACCGCGCGATAATTTATCTTAGTTTGGCGCTATATTTTG	4320
4261	ATCTAGTAAACATAATGACACCGCGCGATAATTTATCTTAGTTTGGCGCTATATTTTG	4320
4321	TTTTCTATCGCTATTAAATGTAATAATGGGGACTCTAATCATATAAAACCCCATCTCAT	4380
4321	TTTTCTATCGCTATTAAATGTAATAATGGGGACTCTAATCATATAAAACCCCATCTCAT	4380
4381	AATAACGTCATCATATACATGTTAATATTATACATGCTTAAACGTAATTCACAGAAATTAT	4440
4381	AATAACGTCATCATATACATGTTAATATTATACATGCTTAAACGTAATTCACAGAAATTAT	4440
4441	ATGATAATCATCCAAAGACCGGCAACAGGATTCAAATCTTAAAGAAACTTTTATGCCAAATG	4500
4441	ATGATAATCATCCAAAGACCGGCAACAGGATTCAAATCTTAAAGAAACTTTTATGCCAAATG	4500
4501	TTTGAACGATCGTTCGTCGAGCTATGGGCCGA	4533
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RESULT 14

US-09-845-064-19

; Sequence 19, Application US/09845064

; Publication No. US20030175976A1

; GENERAL INFORMATION:

; APPLICANT: MERISTEM THERAPEUTICS

; TITLE OF INVENTION: CLEAN SYNTHETIC VECTORS, PLASMIDS, TRANSGENIC PLANTS

; TITLE OF INVENTION: AND PLANT PARTS CONTAINING SAID VECTORS, AND THEIR

; TITLE OF INVENTION: METHODS OF PRODUCTION

; FILE REFERENCE: SynVec1

; CURRENT APPLICATION NUMBER: US/09/845, 064

; CURRENT FILING DATE: 2001-04-27

; NUMBER OF SEQ ID NOS: 57

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 19

; LENGTH: 7503

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:Plasmid

; OTHER INFORMATION: pMRT1205

; FEATURE:

; NAME/KEY: rep\_origin

; LOCATION: (1)..(654)

; OTHER INFORMATION: Origin of replication ori RK2

; FEATURE:

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/ NAME/KEY: rep origin
/ LOCATION: (655)..(1263)
/ OTHER INFORMATION: Origin of replication ori ColeI
/ FEATURE:
/ NAME/KEY: gene
/ LOCATION: (1264)..(2603)
/ OTHER INFORMATION: NPT III gene coding for neomycin
/ OTHER INFORMATION: phosphotransferase and kanamycin resistance
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (2604)..(4098)
/ OTHER INFORMATION: TrfA locus from RK2 coding for two proteins, P285
/ OTHER INFORMATION: and P382, enabling the increase in the replication
/ OTHER INFORMATION: rate
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (4106)..(4271)
/ OTHER INFORMATION: T-DNA left border
/ FEATURE:
/ NAME/KEY: terminator
/ LOCATION: (4272)..(4559)
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/ NAME/KEY: gene
/ LOCATION: (4560)..(5559)
/ OTHER INFORMATION: NPT II gene coding for neomycin phosphotransferase
/ OTHER INFORMATION: and kanamycin resistance
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/ NAME/KEY: promoter
/ LOCATION: (5560)..(5771)
/ OTHER INFORMATION: No. US20030175976Alaline synthetase promoter
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/ LOCATION: (5772)..(6514)
/ OTHER INFORMATION: Enhanced promoter from 35S ribosome
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (6514)..(6566)
/ OTHER INFORMATION: MCS multiple cloning site
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/ NAME/KEY: polyA signal
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/ OTHER INFORMATION: Poly A from 35S ribosome
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (7296)..(7323)
/ OTHER INFORMATION: MCS multiple cloning site
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (7323)..(7496)
/ OTHER INFORMATION: T-DNA right border
/ US-09-845-064-19
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Query Match          94.3%; Score 4531.4; DB 10; Length 7503;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4532; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1  CCGGGCTGGTTGCCCTCGCCGCTGGGCTGGCGCGCGTCTATGGCCCTGCAAAACGGCCAG 60
Db      1  CCGGGCTGGTTGCCCTCGCCGCTGGGCTGGCGCGCGTCTATGGCCCTGCAAAACGGCCAG 60

Qy      61  AAACCGCGTGAAGCGGTGTCGAGACACCCGCGCGCGCGGTGTGGATACCTCGGG 120
Db      61  AAACCGCGTGAAGCGGTGTCGAGACACCCGCGCGCGCGGTGTGGATACCTCGGG 120

Qy      121  AAAACTTGGCCCTCACTGACAGATGAGGGCGGAGTTGACACTTGAAGGCGCCACTCAC 180
Db      121  AAAACTTGGCCCTCACTGACAGATGAGGGCGGAGTTGACACTTGAAGGCGCCACTCAC 180

Qy      181  CCGCGCGCGGCTTGACAGATGAGGGCGAGGCTCGATTTCCGCGCGGCGACGTGGAGCTGGC 240
Db      181  CCGCGCGCGGCTTGACAGATGAGGGCGAGGCTCGATTTCCGCGCGGCGACGTGGAGCTGGC 240
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Qy      241  CAGCCTCGCAAAATCGCGCAAAAACGCTGATTTTACGCGAGTTTCCACAGATGATGTGA 300
Db      241  CAGCCTCGCAAAATCGCGCAAAAACGCTGATTTTACGCGAGTTTCCACAGATGATGTGA 300

Qy      301  CAAGCCTGGGATAAGTGCCTTGGGTATGACACTTGAAGGGCGCGACTACTGACAGAT 360
Db      301  CAAGCCTGGGATAAGTGCCTTGGGTATGACACTTGAAGGGCGCGACTACTGACAGAT 360

Qy      361  GAGGGCGCGATCCTTTGACACTTGAAGGGCGAGTGTCTCAGAGATGAGGGCGCACCTAT 420
Db      361  GAGGGCGCGATCCTTTGACACTTGAAGGGCGAGTGTCTCAGAGATGAGGGCGCACCTAT 420

Qy      421  TGACATTTGAGGGGCTGTCCACAGGCGAGAAAATCCAGCATTTTCAAGGGTTTCCGGCCGT 480
Db      421  TGACATTTGAGGGGCTGTCCACAGGCGAGAAAATCCAGCATTTTCAAGGGTTTCCGGCCGT 480

Qy      481  TTTTTCGGCACCGCTAACCTGTCTTTTAACCTGCTTTTAAACCAATATTTATAAACCCTG 540
Db      481  TTTTTCGGCACCGCTAACCTGTCTTTTAAACCTGCTTTTAAACCAATATTTATAAACCCTG 540

Qy      541  TTTTAAACAGGGCTCGCCCTGTGCGGTGACCGCGCACGCGAAGGGGGTGCCTCCCC 600
Db      541  TTTTAAACAGGGCTCGCCCTGTGCGGTGACCGCGCACGCGAAGGGGGTGCCTCCCC 600

Qy      601  CTTTCTCGAAACCTTCCCGGAAAGGTATGCGGTGTGAAATACCGCACAGATGCGTAAGAGA 660
Db      601  CTTTCTCGAAACCTTCCCGGAAAGGTATGCGGTGTGAAATACCGCACAGATGCGTAAGAGA 660

Qy      661  AAATACCGCATCAGGGCGCTTCCGGTTCCTCGCTCACTGACTCGCTCGGCTCGGTGTT 720
Db      661  AAATACCGCATCAGGGCGCTTCCGGTTCCTCGCTCACTGACTCGCTCGGCTCGGTGTT 720

Qy      721  CGGCTGGCGGAGCGGTATCAGCTCACTCAAAGGGGTAAATACGTTTATCCACAGAAATCA 780
Db      721  CGGCTGGCGGAGCGGTATCAGCTCACTCAAAGGGGTAAATACGTTTATCCACAGAAATCA 780

Qy      781  GGGGATAAAGCAGGAAAGAACATGTGAGCAAAAAGGCCAGCAAAAGGCCAGAAACCGTAAA 840
Db      781  GGGGATAAAGCAGGAAAGAACATGTGAGCAAAAAGGCCAGCAAAAGGCCAGAAACCGTAAA 840

Qy      841  AAGGCGCGGTGCTGGGTTTTTCCATAGGCTCGGCCCTCGCCCTCGAGGATCAAAAAT 900
Db      841  AAGGCGCGGTGCTGGGTTTTTCCATAGGCTCGGCCCTCGCCCTCGAGGATCAAAAAT 900

Qy      901  CGAGCTCAAGTCAGAGTGGCGAAACCCGACAGGACTATAAAGATACACGAGGTTTCCC 960
Db      901  CGAGCTCAAGTCAGAGTGGCGAAACCCGACAGGACTATAAAGATACACGAGGTTTCCC 960

Qy      961  CTTGGAAGCTCCCTCGTGGCGCTCTCCTGTTCCGACCTGCGCTTACCAGATACCTGTCC 1020
Db      961  CTTGGAAGCTCCCTCGTGGCGCTCTCCTGTTCCGACCTGCGCTTACCAGATACCTGTCC 1020

Qy      1021  GCCTTTCTCCCTTCGGGAACGCTGGCGCTTTCTCATAGCTCAGCTGTAGGTATCTCAGT 1080
Db      1021  GCCTTTCTCCCTTCGGGAACGCTGGCGCTTTCTCATAGCTCAGCTGTAGGTATCTCAGT 1080

Qy      1081  TCGGTGTAGTGTGCTTCCGCTTCAAGCTGGGTGTGTCAGCAAAACCCCGCTTCAGCCCGAC 1140
Db      1081  TCGGTGTAGTGTGCTTCCGCTTCAAGCTGGGTGTGTCAGCAAAACCCCGCTTCAGCCCGAC 1140

Qy      1141  CGCTGCGCTTATCCGTAACCTATCGTCTTGAAGTCCAAACCCGGTAAAGACAGACTTATCG 1200
Db      1141  CGCTGCGCTTATCCGTAACCTATCGTCTTGAAGTCCAAACCCGGTAAAGACAGACTTATCG 1200

Qy      1201  CCACTGCGAGCGCTTCTACCATATATCCCGATTAACCCAGCGAACCATTTGAGGTGAT 1260
Db      1201  CCACTGCGAGCGCTTCTACCATATATCCCGATTAACCCAGCGAACCATTTGAGGTGAT 1260

Qy      1261  AGTTAAGATTTATCCGAGGTATGAAACAGAAATGGACCTTTACAGAAATTTACTCTATGA 1320
Db      1261  AGTTAAGATTTATCCGAGGTATGAAACAGAAATTTGGACCTTTTACAGAAATTTACTCTATGA 1320

Qy      1321  AGCGCCATATTTAAAAAGCTACCAAGACGAAGAGGATGAAGAGGATGAGGAGGAGGATTTG 1380
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Db 1321 AGCCCCATATTTAAAGCTACCAAGACGAAGAGGATGAAGAGATGAGGAGCAGATTG 1380  
QY 1381 CCTTGAATATATTGACAACTACTGATAAGATAAATACATCTTTTATATAGAGATATCGCG 1440  
Db 1381 CCTTGAATATATTGACAACTACTGATAAGATAAATACATCTTTTATATAGAGATATCGCG 1440  
QY 1441 TATGTAAAGATTTGAGGGGCAAGGCATAGGCGCGCTTATCAATATATCTATAGAAT 1500  
Db 1441 TATGTAAAGATTTGAGGGGCAAGGCATAGGCGCGCTTATCAATATATCTATAGAAT 1500  
QY 1501 GGGCAAGCATATAAACTTCATGGACTAATGCTTGAACCCAGGACATAAACCCTTATAG 1560  
Db 1501 GGGCAAGCATATAAACTTCATGGACTAATGCTTGAACCCAGGACATAAACCCTTATAG 1560  
QY 1561 CTTGTAAATTTCTACCAAAATTTGCTTTCAAAATCGSCTCCGTCGATACCTATGTATACG 1620  
Db 1561 CTTGTAAATTTCTACCAAAATTTGCTTTCAAAATCGSCTCCGTCGATACCTATGTATACG 1620  
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Db 1621 CCAACTTTGAAAAACACTTTGAAAAAGCTGTTTTCTGGTATTTAAAGTTTTAGAATGCAA 1680  
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Db 1681 GGAACAGTGAATTTGGAGTTTCGTCTGTATATAATTAGCTTCTGGGATATCTTTAAATACT 1740  
QY 1741 GTAGAAAGAGGAGGAATAATAAATGCGCTAAATGAGATATACCCGGAATTTGAAAA 1800  
Db 1741 GTAGAAAGAGGAGGAATAATAAATGCGCTAAATGAGATATACCCGGAATTTGAAAA 1800  
QY 1801 ACTGATCGAAAAATACCGCTGCGTAAAGATACGGAAGGAATGTCTCTCTAAGGTATA 1860  
Db 1801 ACTGATCGAAAAATACCGCTGCGTAAAGATACGGAAGGAATGTCTCTCTAAGGTATA 1860  
QY 1861 TAAAGCTGGTGGGAGAAAACTATATTTAAAAATGACGGAAGCGGTATAAAGG 1920  
Db 1861 TAAAGCTGGTGGGAGAAAACTATATTTAAAAATGACGGAAGCGGTATAAAGG 1920  
QY 1921 GACCACCTATGATGTGAACGGAAGGAAGGACATGATGCTATGCTGGAAGGAAGCTGCC 1980  
Db 1921 GACCACCTATGATGTGAACGGAAGGAAGGACATGATGCTATGCTGGAAGGAAGCTGCC 1980  
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QY 2041 GGCCGATGGCGTCTTTGCTCGGAAGAGTATGAAGATGAACAAAGCCCTGAAAAGATTAT 2100  
Db 2041 GGCCGATGGCGTCTTTGCTCGGAAGAGTATGAAGATGAACAAAGCCCTGAAAAGATTAT 2100  
QY 2101 CGAGCTGTATGGGAGTGCATAGGCTTTTCACTCATCGACATATCGGATTTGCCCTA 2160  
Db 2101 CGAGCTGTATGGGAGTGCATAGGCTTTTCACTCATCGACATATCGGATTTGCCCTA 2160  
QY 2161 TACGAATAGCTTACAGACGCGCTTAGCCGAATTTGGATTACTTACTGAATAACCATCTGCC 2220  
Db 2161 TACGAATAGCTTACAGACGCGCTTAGCCGAATTTGGATTACTTACTGAATAACCATCTGCC 2220  
QY 2221 CGATGTGGATTTGGGAAACCTGGGAAAGACACTCCATTTAAAGATCCCGCGAGCTGTA 2280  
Db 2221 CGATGTGGATTTGGGAAACCTGGGAAAGACACTCCATTTAAAGATCCCGCGAGCTGTA 2280  
QY 2281 TGATTTTTTAAAGACGGAAGCCCGAAGAGGAACCTTGTCTTTTCCACGCGACCTGGG 2340  
Db 2281 TGATTTTTTAAAGACGGAAGCCCGAAGAGGAACCTTGTCTTTTCCACGCGACCTGGG 2340  
QY 2341 AGACAGCAACATCTTTGTGAAGATGCGCAAGTAAAGTGGCTTTATTTGATCTTGGGAGAG 2400  
Db 2341 AGACAGCAACATCTTTGTGAAGATGCGCAAGTAAAGTGGCTTTATTTGATCTTGGGAGAG 2400  
QY 2401 CGGCAGGGCGGACAAGTGGTATGACATTTGCTGCTCCGCTCGATCAGGAGGATAT 2460

Db 2401 CGGCAGGGCGGACAAAGTGGTATGACATTTGCTTCTCGCTCCGTCGATCAGGAGGATAT 2460  
QY 2461 CGGGGAAGAACAGTATGTGAGCTATTTTTCATCTTACTGGGATCAAGCTCATTTGGGA 2520  
Db 2461 CGGGGAAGAACAGTATGTGAGCTATTTTTCATCTTACTGGGATCAAGCTCATTTGGGA 2520  
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Db 2521 GAAAAATAAATAATATATTTTACTGATGAAATTTGTTTTAGTACTAGATGTGGCGCAACG 2580  
QY 2581 ATGCCCGGCACAGCAGGAGCGCACCGACTTCTTCCGATCAAGTGTTTTGGCTCTCAGG 2640  
Db 2581 ATGCCCGGCACAGCAGGAGCGCACCGACTTCTTCCGATCAAGTGTTTTGGCTCTCAGG 2640  
QY 2641 CCAGAGCCCAACGGCAAGTATTTTGGCAAGGGGTGCTGGTATTTCTGTCAGGGCAAGATTC 2700  
Db 2641 CCAGAGCCCAACGGCAAGTATTTTGGCAAGGGGTGCTGGTATTTCTGTCAGGGCAAGATTC 2700  
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Db 2821 CCCCGCGTGAAGTGGGGCAATCCCACAAAGGAGGGTGAATGAATCGGACGTTTTGACCGGA 2880  
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Db 2881 AGSCATACAGGCAAGAACTGATCGACGCGGGGTTTTCCGCGAGGATGCCAAACCATCG 2940  
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Db 2941 CAAGCCGACCGCTCATGCTGCGCCCGCGGAAACCTTCCAGTCCGCTCGGCTCGATGGTCC 3000  
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Qy 3901 TGAAGAAAGTGGCGGACAGGTGCGGGAAGCTCGGAAGAGTTGCGAGGAGCGGCTGG 3960
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Db 3961 TGAACACGCTGGGTCAATGATGACCTGGTGCAATTCGAAACGCTAGGGCTTGTGGGGT 4020
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Db 4081 CTGATGGGCTGCCTGTATCAGATGGTGATTTTGTGCGGAGCTGCGGTGCGGGAGCTGTT 4140
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Qy 4441 ATGATAATCATCGCAAGACCGGCAACAGGATTCATCTTAAGAACTTTATGCAAAATG 4500
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Qy 4501 TTTTGAACGATCGTTCGTGAGCTATGGGCCGA 4533
Db 4501 TTTTGAACGATCGTTCGTGAGCTATGGGCCCAA 4533
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RESULT 15

US-09-845-064-55

; Sequence 55, Application US/09845064

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; Publication No. US20030175976A1
; GENERAL INFORMATION:
; APPLICANT: MERISTEM THERAPEUTICS
; TITLE OF INVENTION: CLEAN SYNTHETIC VECTORS, PLASMIDS, TRANSGENIC PLANTS
; TITLE OF INVENTION: AND PLANT PARTS CONTAINING SAID VECTORS, AND THEIR
; FILE REFERENCE: METHODS OF PRODUCTION
; FILE REFERENCE: SynVec1
; CURRENT APPLICATION NUMBER: US/09/845,064
; CURRENT FILING DATE: 2001-04-27
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 55
; LENGTH: 8289
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: pMRT1337
; NAME/KEY: misc_feature
; LOCATION: (1)
; OTHER INFORMATION: pMRT1337 was obtained from the insertion, into
; OTHER INFORMATION: pMRT1205, of the gfp gene isolated from
; OTHER INFORMATION: pBINm-gfpS-ER
; US-09-845-064-55
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Query Match 94.3%; Score 4531.4; DB 10; Length 8289;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4532; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 1 CCGGGCTGGTTGGCCCTCGCGCTGGGCTGGCGGCGCTCTATGGCCCTGCAAGCGCCAG 60
Qy 61 AAACGCGCTCGAAGCCGTGTGCGAGACACCGCGCGCGCGCTTGTGGATACCTCGCG 120
Db 61 AAACGCGCTCGAAGCCGTGTGCGAGACACCGCGCGCGCGCTTGTGGATACCTCGCG 120
Qy 121 AAAAATTTGGCCCTCACTGACAGATGAGGGCGGACGTTGACACTTGAGGGGCGGACTCAC 180
Db 121 AAAAATTTGGCCCTCACTGACAGATGAGGGCGGACGTTGACACTTGAGGGGCGGACTCAC 180
Qy 181 CCGGCGCGGCTTGACAGATGAGGGCGGACGCTCGATTTTCGGCCGCGGACGCTGGAGCTGGC 240
Db 181 CCGGCGCGGCTTGACAGATGAGGGCGGACGCTCGATTTTCGGCCGCGGACGCTGGAGCTGGC 240
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Db 241 CAGCCTCGCAAAATCGCGGAAACCGCTGATTTTACCGAGTTTCCACAGATGATGGA 300
Qy 301 CAAGCCTGGGGATAAGTGCCTCGGTATTGACACTTGAGGGGCGGACTACTGACAGAT 360
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Qy 361 GAGGGCGGATCCTTGACACTTTGAGGGCGAGAGTGTGACAGATGAGGGGCGGACCTAT 420
Db 361 GAGGGCGGATCCTTGACACTTTGAGGGCGAGAGTGTGACAGATGAGGGGCGGACCTAT 420
Qy 421 TGACATTTGAGGGGCTGTCCACAGGAGAAATCCAGCATTTTGCAGGGTTTCCGCCGT 480
Db 421 TGACATTTGAGGGGCTGTCCACAGGAGAAATCCAGCATTTTGCAGGGTTTCCGCCGT 480
Qy 481 TTTTGGCCACCGCTAACCTGTCTTTTAACTCTGTTTAAACCAATATTTTAAACCTTG 540
Db 481 TTTTGGCCACCGCTAACCTGTCTTTTAACTCTGTTTAAACCAATATTTTAAACCTTG 540
Qy 541 TTTTAAACAGGGCTGCGCCCTGTGCGGTGACCGGCGACCGGAGGGGGTGCCCGCC 600
Db 541 TTTTAAACAGGGCTGCGCCCTGTGCGGTGACCGGCGACCGGAGGGGGTGCCCGCC 600
Qy 601 CTTTCTCGAACCCCTCCCGGAAAGGATGCGGTGTGAAATACCGCACAGATCGGTAAGAGA 660
Db 601 CTTTCTCGAACCCCTCCCGGAAAGGATGCGGTGTGAAATACCGCACAGATCGGTAAGAGA 660
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Qy	661	AAATACCGCATCAGGCGCTCTTCGGCTTCCTCGCTCTCACTGACTCGCTCGCTCGGTCGTT	720
Db	661	AAATACCGCATCAGGCGCTCTTCGGCTTCCTCGCTCTCACTGACTCGCTCGGTCGTT	720
Qy	721	CGGCTGGCGAGCGGTATCAGCTCACTCAAGCGGTATACGGTTATCCACAGATCA	780
Db	721	CGGCTGGCGAGCGGTATCAGCTCACTCAAGCGGTATACGGTTATCCACAGATCA	780
Qy	781	GGGGATAACCGAGAAAGACATGTGAGCAAAAAGGCGCAGCAAAAGGCGCAGGAAACCGTAAA	840
Db	781	GGGGATAACCGAGAAAGACATGTGAGCAAAAAGGCGCAGCAAAAGGCGCAGGAAACCGTAAA	840
Qy	841	AAGCGCGGTTGCTGGCGTTTTTCATPAGGCTCGCCCCCTCGACGAGCATCAAAAAAT	900
Db	841	AAGCGCGGTTGCTGGCGTTTTTCATPAGGCTCGCCCCCTCGACGAGCATCAAAAAAT	900
Qy	901	CGAGCTCAAGTCAGAGGTGGGAAACCCGACAGGACTATAAGATACACAGGCGTTTCCC	960
Db	901	CGAGCTCAAGTCAGAGGTGGGAAACCCGACAGGACTATAAGATACACAGGCGTTTCCC	960
Qy	961	CCTGGAAGCTCCCTCGTGCCTCTCTCTGTTCCGACCCCTCGGCTTACCGGATACCTGTCC	1020
Db	961	CCTGGAAGCTCCCTCGTGCCTCTCTCTGTTCCGACCCCTCGGCTTACCGGATACCTGTCC	1020
Qy	1021	GCCTTTCTCCCTTCGGGAAAGGTGGCGCTTCTCATAGCTCAACGCTGATAGTATCTCAGT	1080
Db	1021	GCCTTTCTCCCTTCGGGAAAGGTGGCGCTTCTCATAGCTCAACGCTGATAGTATCTCAGT	1080
Qy	1081	TCGGTGTAGTTCGTTCCGCTCCAGCTGGGCTGTGTGCACGAAACCCCGCTTCAGCCCGAC	1140
Db	1081	TCGGTGTAGTTCGTTCCGCTCCAGCTGGGCTGTGTGCACGAAACCCCGCTTCAGCCCGAC	1140
Qy	1141	CGCTGCGCTTATCCGGTAACCTATCGTCTTGAGTCCAAACCCGGTAAAGACACGACTTATCG	1200
Db	1141	CGCTGCGCTTATCCGGTAACCTATCGTCTTGAGTCCAAACCCGGTAAAGACACGACTTATCG	1200
Qy	1201	CCACTGGCAGCGCTTCTACCATAAATCCGCGATAAACCCAGCGAACCATTGAGGTGAT	1260
Db	1201	CCACTGGCAGCGCTTCTACCATAAATCCGCGATAAACCCAGCGAACCATTGAGGTGAT	1260
Qy	1261	AGGTAAGATTATCCGAGGTATGAAAACGAGAAATTGGACCTTTACAGAAATTACTCTATGA	1320
Db	1261	AGGTAAGATTATCCGAGGTATGAAAACGAGAAATTGGACCTTTACAGAAATTACTCTATGA	1320
Qy	1321	AGCGCCATATTTAAAAGCTACCAAGACGAAGAGGTGAAGAGATGAGGAGGACAGATTG	1380
Db	1321	AGCGCCATATTTAAAAGCTACCAAGACGAAGAGGTGAAGAGATGAGGAGGACAGATTG	1380
Qy	1381	CCTTGAATATATTGACAAATCTGATAGATAATACATCTTTTATATAGAAAGATATCGCCG	1440
Db	1381	CCTTGAATATATTGACAAATCTGATAGATAATACATCTTTTATATAGAAAGATATCGCCG	1440
Qy	1441	TATGTAAGATTATCAGGGGCAAGGCATAGGAGCGCGCTTATCAATATCTATAGAAAT	1500
Db	1441	TATGTAAGATTATCAGGGGCAAGGCATAGGAGCGCGCTTATCAATATCTATAGAAAT	1500
Qy	1501	GGGCAAGCATAAAACTTCATGGAATAATGCTTGAACCCAGGCAATAAACCTTATAG	1560
Db	1501	GGGCAAGCATAAAACTTCATGGAATAATGCTTGAACCCAGGCAATAAACCTTATAG	1560
Qy	1561	CTTGTAAATTTCTACCAAAATTTGTGGTTTCAAAATCGGCTCCGTCGATCTATGTTATACG	1620
Db	1561	CTTGTAAATTTCTACCAAAATTTGTGGTTTCAAAATCGGCTCCGTCGATCTATGTTATACG	1620
Qy	1621	CCAACTTTGAAAAACACTTTTGAAGAAAGCTGTTTTCTGGTATTTAAGGTTTTAGAAATGCAA	1680
Db	1621	CCAACTTTGAAAAACACTTTTGAAGAAAGCTGTTTTCTGGTATTTAAGGTTTTAGAAATGCAA	1680
Qy	1681	GGACAGTGAATTTGGAGTTCGTTGTTATAATAGCTTCTGGGGTATCTTTAAATACT	1740
Db	1681	GGACAGTGAATTTGGAGTTCGTTGTTATAATAGCTTCTGGGGTATCTTTAAATACT	1740
Qy	1741	GTAGAAAAGAGGAGGAAATAATAAATGGCTAAATAAGAGATATACCCGGAAATTGAAAAA	1800

Db	1741	GTAGAAAAGAGGAGGAAATAATAAATGGCTAAATAAGAGATATACCCGGAAATTGAAAAA	1800
Qy	1801	ACTGATCGAAAAATACCGCTGCGTAAAGATACGGAAGGAATGTCTCTCTCAAGGTATA	1860
Db	1801	ACTGATCGAAAAATACCGCTGCGTAAAGATACGGAAGGAATGTCTCTCTCAAGGTATA	1860
Qy	1861	TAACTGGTGGGAGAAAAATGAAACCTTATATTTAAAAATGACGAGACCGCGTATAAAGG	1920
Db	1861	TAACTGGTGGGAGAAAAATGAAACCTTATATTTAAAAATGACGAGACCGCGTATAAAGG	1920
Qy	1921	GACCACTATGATGTCGAACGGGAAAAAGNACATGATGCTATGCTGGAAGGAAAGCTGGCC	1980
Db	1921	GACCACTATGATGTCGAACGGGAAAAAGNACATGATGCTATGCTGGAAGGAAAGCTGGCC	1980
Qy	1981	TGTTCCAAAGGCTCCTCACCTTTGAAACGGCATGATGCTGGAGCAATCTGCTCATGAGTGA	2040
Db	1981	TGTTCCAAAGGCTCCTGCACTTTGAAACGGCATGATGCTGGAGCAATCTGCTCATGAGTGA	2040
Qy	2041	GGCCGATGGCGTCTTTTGCTCGGAAGAGTATGAAGATGAACAAAGCCCTGAAAAGATTAT	2100
Db	2041	GGCCGATGGCGTCTTTTGCTCGGAAGAGTATGAAGATGAACAAAGCCCTGAAAAGATTAT	2100
Qy	2101	CGAGCTGTATCGGAGTGCATCAGGCTCTTTCACTCGATCGACATATCGGATTTGCCCTA	2160
Db	2101	CGAGCTGTATCGGAGTGCATCAGGCTCTTTCACTCGATCGACATATCGGATTTGCCCTA	2160
Qy	2161	TACGAATAGCTTAGACAGCGCTTTAGCCGAATTTGGATTTACTTACTGAATAACCATCTGGC	2220
Db	2161	TACGAATAGCTTAGACAGCGCTTTAGCCGAATTTGGATTTACTTACTGAATAACCATCTGGC	2220
Qy	2221	CGATGTGGATTGCGAAAACTGGGAAAGAACACTCCATTTAAAGATCCCGCGAGCTGTA	2280
Db	2221	CGATGTGGATTGCGAAAACTGGGAAAGAACACTCCATTTAAAGATCCCGCGAGCTGTA	2280
Qy	2281	TGATTTTAAAGACGGAAGAAAGCCGAAAGAGAACCTTTGCTTTTCCGACGCGACCTGGG	2340
Db	2281	TGATTTTAAAGACGGAAGAAAGCCGAAAGAGAACCTTTGCTTTTCCGACGCGACCTGGG	2340
Qy	2341	AGACACACATCTTTTGTAAGATGCAAAAGTAAGTGGCTTTTATGATCTCGGAGAAAG	2400
Db	2341	AGACACACATCTTTTGTAAGATGCAAAAGTAAGTGGCTTTTATGATCTCGGAGAAAG	2400
Qy	2401	CGGACGGGGGCAACAGTGGTATGACATTCGCTTCGCGTCCGCTCGATCAGGAGGATAT	2460
Db	2401	CGGACGGGGGCAACAGTGGTATGACATTCGCTTCGCGTCCGCTCGATCAGGAGGATAT	2460
Qy	2461	CGGGGAAGAACAGTATGTGAGCTATTTTGTACTTACTGGGATCAAGCTGATTTGGGA	2520
Db	2461	CGGGGAAGAACAGTATGTGAGCTATTTTGTACTTACTGGGATCAAGCTGATTTGGGA	2520
Qy	2521	GAATAAATAATATATTTTACTGATGAAATGTTTGTAGTACCTAGATGTGGCGAACG	2580
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Qy	2581	ATGCCGGGCAACAGAGGAGCGCACCGACTTCTTCGCGCATCAAGTGTTTTGGCTCTCAGG	2640
Db	2581	ATGCCGGGCAACAGAGGAGCGCACCGACTTCTTCGCGCATCAAGTGTTTTGGCTCTCAGG	2640
Qy	2641	CGAGGCCCAACGCAAGTATTTGGGCAAGGGGTGCTGGTATTTGTCGAGGGCAAGATTC	2700
Db	2641	CGAGGCCCAACGCAAGTATTTGGGCAAGGGGTGCTGGTATTTGTCGAGGGCAAGATTC	2700
Qy	2701	GGNATACCAAGTACGAGAGGAGCGCGACCGCTACCGGACCGACTTCAATTTGCCGATA	2760
Db	2701	GGNATACCAAGTACGAGAGGAGCGCGACCGCTACCGGACCGACTTCAATTTGCCGATA	2760
Qy	2761	AGGTGATTTATCTGGACACCAAGGACACGAGGCGGTCAAATCAGGAATAAGGSCACATTG	2820
Db	2761	AGGTGATTTATCTGGACACCAAGGACACGAGGCGGTCAAATCAGGAATAAGGSCACATTG	2820
Qy	2821	CCCGCGCTGAGTTCGGGGCAATCCCGCAAGGAGGGTGAATGAATCGGACGTTTTCACCGGA	2880

Db 2821 CCCCCGCTGAGTCGGGGCAATCCCGCAAGAGGGTGAATGAATCGGACGCTTTTGACCGGA 2880  
Qy 2881 AGGCATACAGGCAAGAACTGATCGACGCGGGGTTTTCCGCCGAGGATGCCGAAACCATCG 2940  
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Qy 3781 AGTACCGCAAGCTGTGCGCGACGCGCCGACGGAATGTTGCACTATTTTTCAGCTCGACCGGG 3840  
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Db 3841 AGCGTACCCGCTCAAGCTGGAACCTTCGCGCTCATGTGCGGATCGGATTCACCCCGCG 3900  
Qy 3901 TGAAGAAGTGGCGAGCAGGTTCGCGAAGCTTCGGAAGAGTTCGAGGCGAGCGGCTGG 3960  
Db 3901 TGAAGAAGTGGCGAGCAGGTTCGCGAAGCTTCGGAAGAGTTCGAGGCGAGCGGCTGG 3960

Qy 3961 TGGAAACACGCCCTGGGTTCAATGATGACCTGGTGCATTGCAAAACGCTAGGCGCTTGTGGGT 4020  
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Qy 4081 CTGATGGGCTGCCCTGTATCGAGTGGTGATTTGTGCGAGCTGCCGCTCGGGAGCTGTT 4140  
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Search completed: July 20, 2004, 11:37:01  
Job time : 1973 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 20, 2004, 11:04:20 ; Search time 11262 Seconds  
(without alignments)  
12740.879 Million cell updates/sec

Title: US-09-845-064-10  
Perfect score: 4805  
Sequence: 1 cgggtgtgtgcctcgcc.....gagcgcttggagcgtca 4805

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues  
Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

- EST.\*
- 1: em\_estba.\*
  - 2: em\_esthum.\*
  - 3: em\_estin.\*
  - 4: em\_estnu.\*
  - 5: em\_estov.\*
  - 6: em\_estpl.\*
  - 7: em\_estro.\*
  - 8: em\_htc.\*
  - 9: gb\_est1.\*
  - 10: gb\_est2.\*
  - 11: gb\_htc.\*
  - 12: gb\_est3.\*
  - 13: gb\_est4.\*
  - 14: gb\_est5.\*
  - 15: em\_estfun.\*
  - 16: em\_estom.\*
  - 17: em\_gss\_hum.\*
  - 18: em\_gss\_inv.\*
  - 19: em\_gss\_pln.\*
  - 20: em\_gss\_vrt.\*
  - 21: em\_gss\_fun.\*
  - 22: em\_gss\_mam.\*
  - 23: em\_gss\_mus.\*
  - 24: em\_gss\_pro.\*
  - 25: em\_gss\_rod.\*
  - 26: em\_gss\_pbg.\*
  - 27: em\_gss\_vrl.\*
  - 28: gb\_gss1.\*
  - 29: gb\_gss2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	547	11.4	954	9	AL044364
2	546.8	11.4	699	14	CB879625
3	544.2	11.3	582	14	CB872328
4	544.2	11.3	604	14	CB872523

5	544.2	11.3	619	29	CG711606
6	544.2	11.3	656	14	CB858283
7	544.2	11.3	669	13	BQ660152
8	544.2	11.3	677	14	CB865829
9	544.2	11.3	695	13	BQ660140
10	544.2	11.3	700	13	BQ660226
11	544.2	11.3	703	9	AJ281437
12	544.2	11.3	863	14	CF752100
13	544.2	11.3	966	28	BZ570738
14	544.2	11.3	996	29	CG392995
15	544.2	11.3	1089	9	AU081124
16	543.4	11.3	925	14	CB686151
17	543.2	11.3	628	14	CB872076
18	543.2	11.3	680	28	BH235176
19	543.2	11.3	687	9	AU001481
20	542.6	11.3	1073	14	CF269652
21	542.6	11.3	1249	28	BZ572284
22	542	11.3	691	14	CB875232
23	541	11.3	1067	9	AU081137
24	541	11.3	1387	28	BZ577525
25	540.6	11.3	1346	28	BZ572730
26	540	11.2	914	28	BZ569398
27	537.8	11.2	1369	28	BZ579291
28	537.6	11.2	565	14	CB871309
29	536.8	11.2	620	14	CB858957
30	536.6	11.2	593	14	CB858509
31	536.4	11.2	1038	28	BZ549934
32	536.2	11.2	1304	28	BZ576307
33	536	11.2	673	14	CB864014
34	536	11.2	835	28	BZ571572
35	536	11.2	1341	28	BZ576229
36	535.2	11.1	567	29	CG707935
37	535.2	11.1	583	14	CB859700
38	535.2	11.1	663	9	AU001472
39	534.6	11.1	906	29	CG839354
40	533.2	11.1	605	14	CB859681
41	533.2	11.1	621	14	CB872402
42	533.2	11.1	649	14	CB859824
43	533.2	11.1	662	14	CB880413
44	533	11.1	896	28	BZ551301
45	533	11.1	902	28	BZ566804

ALIGNMENTS

RESULT 1  
AL044364  
LOCUS  
DEFINITION DKFZp434C172 sl 434 (synonym: htesa) Homo sapiens cDNA clone  
954 bp mRNA linear EST 04-SEP-2003  
ACCESSION AL044364  
VERSION AL044364.1  
KEYWORDS GI:5432586  
SOURCE EST.  
ORGANISM Homo sapiens (human)

REFERENCE 1 (bases 1 to 954)  
AUTHORS Ansoorge,W., Benes,V., Krieger,S., Mewes,H.W., Gassenhuber,J. and Wiemann,S.

TITLE EST (Ansoorge, Benes, et al.)  
JOURNAL Unpublished (1999)  
COMMENT Contact: MIPS

MIPS  
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany  
This is the 3' sequence of the clone insert  
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer  
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;  
sequenced by EMBL (European Molecular Biology Laboratories,  
Heidelberg/Germany) within the cDNA sequencing consortium of the  
German Genome Project.  
No r1 sequence available.

CG711606 1119022A1  
CB858283 HI06H04W  
BQ660152 HI01D08W  
CB865829 HD10N11W  
BQ660140 HI01C11W  
BQ660226 HI01J04W  
AJ281437 4A3A-P4C3  
CF752100 TGD9 Hum  
BZ570738 meh2\_1513  
CG392995 ZMMBC000  
AU081124 AU081124  
CB686151 Bn01b\_02o  
CB872076 HC06H19y  
BH235176 PS\_00.x S  
AU001481 AU001481  
CF269652 FCylcolD8  
BZ572284 meh2\_2572  
CB875232 HK07K20W  
AU081137 AU081137  
BZ577525 meh2\_545.  
BZ572730 meh2\_2771  
BZ569398 pac82-164  
BZ579291 meh2\_6285  
CB871309 HC03J21Y  
CB858957 HI08N12W  
CB858509 HI07E22W  
BZ576307 pac81-60  
CB864014 HH07L14Y  
BZ571572 meh2\_1950  
BZ576229 meh2\_4835  
CG707935 1119004D1  
CB859700 HI1E22W  
AU001472 AU001472  
CG839354 ZMMBC021  
CB859681 HI1D22W  
CB872402 HC07N16Y  
CB859824 HI1L13W  
CB880413 HM06H11W  
BZ551301 pac81-60  
BZ566804 pac82-167

This clone (DKFZp434C172) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzd.de.

## FEATURES

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## ORIGIN

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Query Match      11.4%; Score 547; DB 9; Length 954;
Best Local Similarity 93.5%; Pred. NO. 2e-114;
Matches 571; Conservative 0; Mismatches 40; Indels 0; Gaps 0;
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161	Db	TCGCGCGCGAATTGCAAGACTCTGCATTAATGAAATCGGCCAACGCGCGGGAGAGCGCGTT	220
665	QY	ACGCGATCAGGCGCTCTTCCGCTTCTTCGCTCACTGACTCGCTCGCTCGCTTCGCTTCGGC	724
221	Db	TGCGTATTGGGCGCTCTTCCGCTTCTTCGCTCACTGACTCGCTCGCTCGCTTCGCTTCGGC	280
725	QY	TGCGGCGAGCGGTTATCAGCTCACTCAAGAGCGGTAAATACGGTTATTCACAGAAATCAGGG	784
281	Db	TGCGGCGAGCGGTTATCAGCTCACTCAAGAGCGGTAAATACGGTTATTCACAGAAATCAGGG	340
785	QY	ATAACGAGGAAAGAACATGTGACGAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGG	844
341	Db	ATAACGAGGAAAGAACATGTGACGAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGG	400
845	QY	CCGCGTTGCTGGCGTTTTTTCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGAC	904
401	Db	CCGCGTTGCTGGCGTTTTTTCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGAC	460
905	QY	GCTCAAGTCAGAGTGGGAAACCCGACAGGACTATAAGATACGAGCGTTTCCCGCTG	964
461	Db	GCTCAAGTCAGAGTGGGAAACCCGACAGGACTATAAGATACGAGCGTTTCCCGCTG	520
965	QY	GAAGCTCCCTCGTSCGCTCTCCTGTTCGACCCCTGCGCTTTACCGGATACCTGTCCGCT	1024
521	Db	GAAGCTCCCTCGTSCGCTCTCCTGTTCGACCCCTGCGCTTTACCGGATACCTGTCCGCT	580
1025	QY	TTCTCCCTTCGGGAAGCGTGGCGTTTCTCATAGCTACGCTGTAGGTATCTCAAGTTCGG	1084
581	Db	TTCTCCCTTCGGGAAGCGTGGCGTTTCTCATAGCTACGCTGTAGGTATCTCAAGTTCGG	640
1085	QY	TGTAGTTCGTTTCGCTCCAGCTGGGCTGTGTGACGAAACCCCGCTTCAGCGCGACCGCT	1144
641	Db	TGTAGTTCGTTTCGCTCCAGCTGGGCTGTGTGACGAAACCCCGCTTCAGCGCGACCGCT	700
1145	QY	GCGCTTTATCCGGTAACTATCGTCTTGAGTCCAAACCCGGTAAAGACAGCACTTATCGCCAC	1204
701	Db	GCGCTTTATCCGGTAACTATCGTCTTGAGTCCAAACCCGGTAAAGACAGCACTTATCGCCAC	760
1205	QY	TGGCAGCAGCC	1215
761	Db	TGGCAGCAGCC	771

## RESULT 2

RESOLUTION 2	CB879625	699 bp	mRNA	linear	EST 23-APR-2003
LOCUS	HP03A17	HP Hordeum vulgare subsp. vulgare	cDNA clone	HP03A17	
DEFINITION	3-PRIME, mRNA sequence.				
ACCESSION	CB879625				
VERSION	CB879625.1	GI:30081611			
KEYWORDS	EST.				

**SOURCE**  
**ORGANISM**

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
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2				
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## FEATURES

source

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/mol_type="mRNA"
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/dev_stage="seedlings grown in greenhouse for 6 days"
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NOTE=Vector: pBluescript SK+; Site_1: EcoRI (5'-end of cDNA); Site_2: XhoI (3'-end of cDNA); Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRI adapter used for cloning. To excise the insert, restriction sites upstream of the EcoRI should be used (e.g. BamHI, SalI, PstI). NOTE: A due to the cloning system used Blue/white selection for recombinants is not 100% reliable.Average insert size 850 bp"

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## ORIGIN

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Query Match      11.4%; Score 546.8; DB 14; Length 699;
Best Local Similarity 95.4%; Pred. No. 2e-114;
Matches 563; Conservative 0; Mismatches 27; Indels 0; Gaps 0;
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Qy	626	TGCGGTCTGAATAACCGCACAGATGCGTATAGGAGAAATACCGCATCAGGCGCTCTCCG	685
Db	38	TGCAATTAATGAATCCGCGCAACGCGCGGTATGGCGCGCTCTCCG	97
Qy	686	CTTCTCGCTCACTGACTCGCTCGGCTCGGTCGGTTCGGCTCGCGAGCGGTATCAGCTC	745
Db	98	CTTCTCGCTCATGACTCGCTGCGCTCGGTCGGTTCGGCTCGCGAGCGGTATCAGCTC	157
Qy	746	ACTCAAAAGGCGGTAAATACGGTTATCCACAGAAATCAGGGGATAAACGAGGAAAGAACATGT	805
Db	158	ACTCAAAAGGCGGTAAATACGGTTATCCACAGAAATCAGGGGATAAACGAGGAAAGAACATGT	217
Qy	806	GAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCTGCTGGCGCTTTTCC	865
Db	218	GAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCTGCTGGCGCTTTTCC	277
Qy	866	ATAGGCTCCGCCCCCTTGACAGAGCATCAAAAAATCGACGCTCAAGTTCAGAGGTGGCGAA	925
Db	278	ATAGGCTCCGCCCCCTTGACAGAGCATCAAAAAATCGACGCTCAAGTTCAGAGGTGGCGAA	337
Qy	926	ACCGCAGAGCATATAAGATACACAGCGCTTCCCCCTGGAAGCTCCCTCGTGGCTCTC	985
Db	338	ACCGCAGAGCATATAAGATACACAGCGCTTCCCCCTGGAAGCTCCCTCGTGGCTCTC	397
Qy	986	CTGTTCGACCCCTGCCGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGG	1045

Db 398 CTGTTCCGACCCCTTACCGGATACCTGTGCCGCTTTTCCCTTCCTCCGGAAGCGTGG 457

Qy 1046 CGCTTTCTCATAGCTACCGTGTAGGTATCTCAGTTCGGTGTAGGTGCTGTTCCGCTCCAAGC 1105

Db 458 CGCTTTCTCATAGCTACCGTGTAGGTATCTCAGTTCGGTGTAGGTGCTGTTCCGCTCCAGC 517

Qy 1106 TGGGCTGTGTGCAGAACCCCGCTTCAGCCGACCGCTCGGCTTATCCGGTAACATATC 1165

Db 518 TGGGCTGTGTGCAGAACCCCGCTTCAGCCGACCGCTCGGCTTATCCGGTAACATATC 577

Qy 1166 GTCTTGAGTCCAAACCGGTAAAGCAGACTTATCGCACCTGGCAGAGCC 1215

Db 578 GTCTTGAGTCCAAACCGGTAAAGCAGACTTATCGCACCTGGCAGAGCC 627

RESULT 3

CB872328

LOCUS CB872328 582 bp mRNA linear EST 03-JUL-2003

DEFINITION HC07102Y CH Hordeum vulgare cDNA clone HC07102 3-PRIME, mRNA

sequence.

CB872328

VERSION CB872328.1 GI:30074308

KEYWORDS EST.

SOURCE Hordeum vulgare

ORGANISM Hordeum vulgare

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Hordeum.

REFERENCE 1 (bases 1 to 582)

AUTHORS Varshney,R.K., Zhang,H., Burton,R., Stein,N., Langridge,P. and Graner,A.

TITLE Barley ESTs from coleoptile tissue

JOURNAL Unpublished (2003)

COMMENT Molecular Markers Group, Department Genbank Institute of Plant Genetics and Crop Plant Research (IPK) Corrensstr. 3, 06466, Gatersleben, Germany Tel: 039482-5522 Fax: 039482-5595 Email: stein@ipk-gatersleben.de Insert Length: 582 Std Error: 0.00 Plate: 7 row: 1 column: 2 Seq primer: SP6.

FEATURES

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/note="Vector: pSPORT; Site 1: SalI (5-end of cDNA); Site 2: NotI (3-end of cDNA); Due to the cloning system used blue/white selection for recombinants is not 100% reliable. Average insert size is 1.3 Kb."

ORIGIN

Query Match 11.3%; Score 544.2; DB 14; Length 582;

Best Local Similarity 99.5%; Pred. No. 7.4e-114;

Matches 546; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 667 CGCATCAGGCGCTCTTCGGTCTTCCTCGCTCACTGCTCGCTCGCTCGCTCGCTGCTG 726

Db 2 CGTATTGGCGCTCTTCGGTCTTCCTCGCTCACTGCTCGCTCGCTCGCTCGCTGCTG 61

Qy 727 CGGGACCGGTATCAGCTCACTCAAGCGGTATACGGTTATCCACAGAAATCAGGGAT 786

Db 62 CGCGACCGGTATCAGCTCACTCAAGCGGTATACGGTTATCCACAGAAATCAGGGAT 121

Qy 787 AACCGAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCC 846

Db 122 AACCGAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCC 181

Qy 847 GCGTTCTCGCGCTTTTCCATAGGCTCCGCCCCCTCGAGAGCATCAAAAAATCGACGC 906

Db 182 GCGTTCTCGCGCTTTTCCATAGGCTCCGCCCCCTCGAGAGCATCAAAAAATCGACGC 241

Qy 907 TCAAGTCAGAGGTGGGAAACCCGACAGGACTATAAAGATACACAGGCGTTTCCCCCTGGA 966

Db 242 TCAAGTCAGAGGTGGGAAACCCGACAGGACTATAAAGATACACAGGCGTTTCCCCCTGGA 301

Qy 967 AGTCCTCTCGTGGCTCTCTGTTTCGACCCCTCGCGCTTACCGGATACCTGTGCGCTTT 1026

Db 302 AGTCCTCTCGTGGCTCTCTGTTTCGACCCCTCGCGCTTACCGGATACCTGTGCGCTTT 361

Qy 1027 CTCCTTCGGGAGCGTGGCGCTTCTCATAGCTCAGCTGTAAGGTATCTCAGTTCCGGTG 1086

Db 362 CTCCTTCGGGAGCGTGGCGCTTCTCATAGCTCAGCTGTAAGGTATCTCAGTTCCGGTG 421

Qy 1087 TAGTCTGTTCCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCTTCAGCCCCGACCGTGC 1146

Db 422 TAGTCTGTTCCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCTTCAGCCCCGACCGTGC 481

Qy 1147 GCCTTATCCGGTAACTATCGTCTTGAGTCCAAACCGGTAAAGACACGACTTATCGCCACTG 1206

Db 482 GCCTTATCCGGTAACTATCGTCTTGAGTCCAAACCGGTAAAGACACGACTTATCGCCACTG 541

Qy 1207 GCAGCAGCC 1215

Db 542 GCAGCAGCC 550

RESULT 4

CB872523

LOCUS CB872523 604 bp mRNA linear EST 03-JUL-2003

DEFINITION HC08007Y CH Hordeum vulgare cDNA clone HC08007 3-PRIME, mRNA

sequence.

CB872523

VERSION CB872523.1 GI:30074503

KEYWORDS EST.

SOURCE Hordeum vulgare

ORGANISM Hordeum vulgare

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Hordeum.

REFERENCE 1 (bases 1 to 604)

AUTHORS Varshney,R.K., Zhang,H., Burton,R., Stein,N., Langridge,P. and Graner,A.

TITLE Barley ESTs from coleoptile tissue

JOURNAL Unpublished (2003)

COMMENT Contact: Stein Nils Molecular Markers Group, Department Genbank Institute of Plant Genetics and Crop Plant Research (IPK) Corrensstr. 3, 06466, Gatersleben, Germany Tel: 039482-5522 Fax: 039482-5595 Email: stein@ipk-gatersleben.de Insert Length: 604 Std Error: 0.00 Plate: 8 row: G column: 7 Seq primer: SP6.

FEATURES

Location/Qualifiers

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Site 2: NotI (3-end of cDNA); Due to the cloning system  
used blue/white selection for recombinants is not 100%  
reliable. Average insert size is 1.3 kb."

ORIGIN	FEATURES									
	source									
	Query Match	11.3%;	Score 544.2;	DB 14;	Length 604;					
	Best Local Similarity	99.5%;	Pred. No. 7.5e-114;							
	Matches 546;	Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0;					
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Qy	727	CGCGAGCGGTATCAGTCTCACTCAAGCGGTAAATACGGTTATCCACAGAATCAGGGAT	786							
Db	62	CGCGAGCGGTATCAGTCTCACTCAAGCGGTAAATACGGTTATCCACAGAATCAGGGAT	121							
Qy	787	AACGAGGAAGACATGTGACCAAGGCGCAAGAGCCAGGACCCGTAAAGGCC	846							
Db	122	AACGAGGAAGACATGTGACCAAGGCGCAAGAGCCAGGACCCGTAAAGGCC	181							
Qy	847	GCCTTGTGCGCTTTTCCATAGGCTCCGCCCTCGACGATCAACAAAATCGACGC	906							
Db	182	GCCTTGTGCGCTTTTCCATAGGCTCCGCCCTCGACGATCAACAAAATCGACGC	241							
Qy	907	TCAAGTCAGAGTGGCGAAACCCGACAGGACTATAAGATACCAAGCGCTTCCCGCTGGA	966							
Db	242	TCAAGTCAGAGTGGCGAAACCCGACAGGACTATAAGATACCAAGCGCTTCCCGCTGGA	301							
Qy	967	AGCTCCCTCGCTCGCTTCTCGTTCGACCCCTCGCTTACCGGATACCTGTCCGCTTT	1026							
Db	302	AGCTCCCTCGCTCGCTTCTCGTTCGACCCCTCGCTTACCGGATACCTGTCCGCTTT	361							
Qy	1027	CTCCCTTCGGAAGCGTGGCGCTTCTCATAGCTCAGCTGTAGTATCTCAGTTCCGGTG	1086							
Db	362	CTCCCTTCGGAAGCGTGGCGCTTCTCATAGCTCAGCTGTAGTATCTCAGTTCCGGTG	421							
Qy	1087	TAGTTCGTTTCGCTCAAGCTGGGTGTGTGACGAAACCCCGCTTACCGCCGACCGCTGC	1146							
Db	422	TAGTTCGTTTCGCTCAAGCTGGGTGTGTGACGAAACCCCGCTTACCGCCGACCGCTGC	481							
Qy	1147	GCCTTATCCGTAATCTCTGAGTCCAAACCCGCTTACGACGACTTATCGCACTG	1206							
Db	482	GCCTTATCCGTAATCTCTGAGTCCAAACCCGCTTACGACGACTTATCGCACTG	541							
Qy	1207	GCAGCAGCC 1215								
Db	542	GCAGCAGCC 550								

RESULT 5  
CG711606  
LOCUS  
DEFINITION 119022A11.xl 1119 - RescueMu Grid AA Zea mays genomic, genomic survey sequence.  
ACCESSION CG711606  
VERSION CG711606.1 GI:37737512  
KEYWORDS GSS.  
SOURCE Zea mays  
ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.  
1 (bases 1 to 619)  
Walbot V.  
Maize genomic sequences found using engineered RescueMu transposon  
Unpublished (2001)  
Contact: Walbot V  
Department of Biological Sciences  
Stanford University  
855 California Ave, Palo Alto, CA 94304, USA  
Tel: 650 723 2227

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Fax: 650 725 8221  
Email: walbot@stanford.edu  
Plate: 1119022 row: 44  
Class: transposon-tagged.  
Location/Qualifiers  
1. .619  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/cultivar="mixed background W23/A188/B73/K55"  
/db\_xref="taxon:4577"  
/tissue\_type="leaf"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_lib="1119 - RescueMu Grid AA"  
/notes="Organ: leaf; Vector: RescueMu (engineered from plusScript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmldb.iastate.edu' and follow the links for 'RescueMu.' Grid AA was grown at UC San Diego in 2002. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

ORIGIN	FEATURES									
	source									
	Query Match	11.3%;	Score 544.2;	DB 29;	Length 619;					
	Best Local Similarity	99.5%;	Pred. No. 7.6e-114;							
	Matches 546;	Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0;					
Qy	667	CGCATCAGAGCGCTTTCGCTTCCTCGCTCACTGACTCGCTCGCTCGCTCGCTCGCTG	726							
Db	20	CGTATTGGGCGCTTTCGCTTCCTCGCTCACTGACTCGCTCGCTCGCTCGCTCGCTG	79							
Qy	727	CGCGAGCGGTATCAGCTCACTCAAAAGCGGTAAATACGGTTATCCACAGAATCAGGGAT	786							
Db	80	CGCGAGCGGTATCAGCTCACTCAAAAGCGGTAAATACGGTTATCCACAGAATCAGGGAT	139							
Qy	787	AACGAGGAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAAACCGTAAAGGCC	846							
Db	140	AACGAGGAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAAACCGTAAAGGCC	199							
Qy	847	GCCTTGTGCGCTTTTCCATAGGCTCCGCCCTCGTACGAGCATCACAAAATCAGCGC	906							
Db	200	GCCTTGTGCGCTTTTCCATAGGCTCCGCCCTCGTACGAGCATCACAAAATCAGCGC	259							
Qy	907	TCAAGTCAGAGTGGCGAAACCCGACGAGACTATAAGATACCAAGCGCTTCCCGCTTGA	966							
Db	260	TCAAGTCAGAGTGGCGAAACCCGACGAGACTATAAGATACCAAGCGCTTCCCGCTTGA	319							
Qy	967	AGCTCCCTCGTTCGCGCTTCTCTGTTCCGAGCCCTCGCGCTTACCGGATACCTGTCCGCTTT	1026							
Db	320	AGCTCCCTCGTTCGCGCTTCTCTGTTCCGAGCCCTCGCGCTTACCGGATACCTGTCCGCTTT	379							
Qy	1027	CTCCCTTCGGAAGCGTGGCGCTTTCTCATAGCTCAGCTGTAGGTATCTCAGTTCCGGTG	1086							
Db	380	CTCCCTTCGGAAGCGTGGCGCTTTCTCATAGCTCAGCTGTAGGTATCTCAGTTCCGGTG	439							
Qy	1087	TAGTTCGTTTCGCTCAAGCTGGGCTGTGTCAGCAACCCCGCTTCCAGCCCGACCGCTGC	1146							
Db	440	TAGTTCGTTTCGCTCAAGCTGGGCTGTGTCAGCAACCCCGCTTCCAGCCCGACCGCTGC	499							
Qy	1147	GCCTTATCCGGAATCTATGCTTTGAGTCCAAACCCCGGTAAGACACGACTTATCGCACTG	1206							
Db	500	GCCTTATCCGGAATCTATGCTTTGAGTCCAAACCCCGGTAAGACACGACTTATCGCACTG	559							
Qy	1207	GCAGCAGCC 1215								
Db	560	GCAGCAGCC 568								

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RESULT 6
CB858283
LOCUS
DEFINITION CB858283 656 bp mRNA linear EST 22-APR-2003
3-PRIME, mRNA sequence.
ACCESSION CB858283
VERSION CB858283.1 GI:30052840
KEYWORDS EST.
SOURCE Hordeum vulgare subsp. vulgare
ORGANISM Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.
1 (bases 1 to 656)
Zhang, H., Weschke, W., Michalek, W., Stein, N. and Graner, A.
EST sequencing and analysis in barley (2002)
Unpublished (2002)
Contact: Stein Nils
Molecular Markers Group, Department Genbank
Institute of Plant Genetics and Crop Plant Research (IPK)
Corrensstr. 3, 06466, Gatersleben, Germany
Tel: 039482-5522
Fax: 039482-5595
Email: stein@ipk-gatersleben.de
Insert Length: 656 Std Error: 0.00
Plate: 6 row: H column: 4
Seq primer: T7.
FEATURES
Location/Qualifiers
1..656
/organism="Hordeum vulgare subsp. vulgare"
/mol_type="mRNA"
/cultivar="barke"
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/db_xref="GABI:555866"
/db_xref="taxon:112509"
/clone="HI06H04"
/tissue_type="female inflorescences"
/dev_stage="female inflorescences (approx. 3 mm in size)"
/lab_host="XL10-Gold"
/clone_lib="HI"
/note="Vector: pBluescript SK+; Site 1: EcoRI (5'-end of
cDNA); Site 2: XhoI (3'-end of cDNA); Due to a cloning
artefact caused by the kit, in most cases the EcoRI site
is NOT present, as well as the EcoRI adapter used for
cloning. To excise the insert, restriction sites upstream
EcoRI should be used (e.g. BamHI, Sali, PstI). NOTE: Also
due to the cloning system used Blue/white selection for
recombinants is not 100% reliable."
ORIGIN
Query Match 11.3%; Score 544.2; DB 14; Length 656;
Best Local Similarity 99.5%; Pred. No. 7.8e-114;
Matches 546; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 667 CGCATCAGCGCTCTTCCGCTTCTCGCTCACTGCTCGCTCGCTCGCTCGCTCGCTCG 726
DB 47 CGTATTGGCGCTCTTCCGCTTCTCGCTCACTGCTCGCTCGCTCGCTCGCTCGCTG 106
QY 727 CGCGGAGCGGTATCAGCTACTCAAAAGCGGTAAATACGGTTATCCACAGAAATCAGGGAT 786
DB 107 CGCGGAGCGGTATCAGCTACTCAAAAGCGGTAAATACGGTTATCCACAGAAATCAGGGAT 166
QY 787 AACGCGAGGAAGAAACATGTGAGCAAAAGCGCAAAAGCGCAAGGAACCGTAAAGAGGC 846
DB 167 AACGCGAGGAAGAAACATGTGAGCAAAAGCGCAAAAGCGCAAGGAACCGTAAAGAGGC 226
QY 847 GCGTTCTGCGGCTTTTCCATAGGCTCCGCCCCCTCGAGGAGCATCACAAAATCGACGC 906
DB 227 GCGTTCTGCGGCTTTTCCATAGGCTCCGCCCCCTCGAGGAGCATCACAAAATCGACGC 286
QY 907 TCAAGTCAGAGGTGGCGAAACCGGACAGGATATAAGATACAGCGGTTTCCCTCTGA 966
DB 287 TCAAGTCAGAGGTGGCGAAACCGGACAGGATATAAGATACAGCGGTTTCCCTCTGA 946

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QY 967 AGCTCCCTCGTGGCTCTCTCTGTTCCGACCCCTCGGCTTACCGGATACCTGTGCGCCTTT 1026
DB 347 AGCTCCCTCGTGGCTCTCTCTGTTCCGACCCCTCGGCTTACCGGATACCTGTGCGCCTTT 406
QY 1027 CTCCTTCCGGGAAGCGTGGCGCTTTCTCATAGCTACGCTGTAGGTATCTCAGTTCCGGTG 1086
DB 407 CTCCTTCCGGGAAGCGTGGCGCTTTCTCATAGCTACGCTGTAGGTATCTCAGTTCCGGTG 466
QY 1087 TAGGTGCTTCCGCTCCAAAGCTGGGCTGTGTGACAGAAACCCCGCTTCAGCCCGACCGCTGC 1146
DB 467 TAGGTGCTTCCGCTCCAAAGCTGGGCTGTGTGACAGAAACCCCGCTTCAGCCCGACCGCTGC 526
QY 1147 GCCTTATCCGCTAACTATCTGTTAGTCCAAACCCCGGTAAAGACACGACTTTATGCCACTG 1206
DB 527 GCCTTATCCGCTAACTATCTGTTAGTCCAAACCCCGGTAAAGACACGACTTTATGCCACTG 586
QY 1207 GCAGCAGCC 1215
DB 587 GCAGCAGCC 595

RESULT 7
BQ660152
LOCUS
DEFINITION BQ660152 669 bp mRNA linear EST 15-JUL-2002
3-PRIME, mRNA sequence.
ACCESSION BQ660152
VERSION BQ660152.1 GI:21801285
KEYWORDS EST.
SOURCE Hordeum vulgare subsp. vulgare
ORGANISM Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.
1 (bases 1 to 669)
Michalek, W., Weschke, W., Pleissner, K.-P. and Graner, A.
EST sequencing and analysis in barley
Unpublished (2000)
Contact: Stein Nils
Molecular Markers Group, Department Genbank
Institute of Plant Genetics and Crop Plant Research (IPK)
Corrensstr. 3, 06466, Gatersleben, Germany
Tel: 039482-5522
Fax: 039482-5595
Email: stein@ipk-gatersleben.de
Insert Length: 669 Std Error: 0.00
Plate: 1 row: D column: 8
Seq primer: T7.
FEATURES
Location/Qualifiers
1..669
/organism="Hordeum vulgare subsp. vulgare"
/mol_type="mRNA"
/cultivar="barke"
/sub_species="vulgare"
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/clone="HI01D08"
/tissue_type="female inflorescences"
/dev_stage="female inflorescences (approx. 3 mm in size)"
/lab_host="XL10-Gold"
/clone_lib="HI"
/note="Vector: pBluescript SK+; Site 1: EcoRI (5'-end of
cDNA); Site 2: XhoI (3'-end of cDNA); Due to a cloning
artefact caused by the kit, in most cases the EcoRI site
is NOT present, as well as the EcoRI adapter used for
cloning. To excise the insert, restriction sites upstream
EcoRI should be used (e.g. BamHI, Sali, PstI). NOTE: Also
due to the cloning system used Blue/white selection for
recombinants is not 100% reliable."
ORIGIN
Query Match 11.3%; Score 544.2; DB 13; Length 669;

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Best Local Similarity 99.5%; Pred. No. 7.8e-114;
Matches 546; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 667 CGCATCAGGCGCTTTCGCTTCTCGCTCAGTCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTG 726
|||
Db 67 CGTATTGGGCGCTTTCGCTTCTCGCTCAGTCTCGCTCGCTCGCTCGCTCGCTCGCTG 126
|||
QY 727 CGCGGAGCGGTATCAGTCTACTCANAAGGCGGTAAATACGGTTATCCACAGAAATCAGGGAT 786
|||
Db 127 CGCGGAGCGGTATCAGTCTACTCANAAGGCGGTAAATACGGTTATCCACAGAAATCAGGGAT 186
|||
QY 787 AACCCAGGAAAGAACATGTGAGCAAAAGGCGCAGCAAAAGGCCAGGAACCCGTAAAGAGGCC 846
|||
Db 187 AACCCAGGAAAGAACATGTGAGCAAAAGGCGCAGCAAAAGGCCAGGAACCCGTAAAGAGGCC 246
|||
QY 847 GCCTTGTGCGCTTTTTCATAGGCTCCGCCGCCCTGACGAGCATCAAAAATTCGACGC 906
|||
Db 247 GCCTTGTGCGCTTTTTCATAGGCTCCGCCGCCCTGACGAGCATCAAAAATTCGACGC 306
|||
QY 907 TCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAGATACCAAGGCTTCCGCCCTGA 966
|||
Db 307 TCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAGATACCAAGGCTTCCGCCCTGA 366
|||
QY 967 AGCTCCCTCGTGGCTCTCTGTTCCGACCTCGCGCTTACCGGATACCTGTCCGCCCTTT 1026
|||
Db 367 AGCTCCCTCGTGGCTCTCTGTTCCGACCTCGCGCTTACCGGATACCTGTCCGCCCTTT 426
|||
QY 1027 CTCCTTTCCGGAAGCGTGGCGCTTTTCATAGTCAAGCTGTAGTATTCAGTTCGGTG 1086
|||
Db 427 CTCCTTTCCGGAAGCGTGGCGCTTTTCATAGTCAAGCTGTAGTATTCAGTTCGGTG 486
|||
QY 1087 TAGGTCTGCTCCAAAGCTGGGCTGTGTGCAAGAACCCCGCTTACGCCGAGCCGCTGC 1146
|||
Db 487 TAGGTCTGCTCCAAAGCTGGGCTGTGTGCAAGAACCCCGCTTACGCCGAGCCGCTGC 546
|||
QY 1147 GCCTTATCCGGTAAGTATCTGTTAGTCCAAACCCGCTTAAGACACGACTTATCGCCACTG 1206
|||
Db 547 GCCTTATCCGGTAAGTATCTGTTAGTCCAAACCCGCTTAAGACACGACTTATCGCCACTG 606
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QY 1207 GCAGCAGCC 1215
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Db 607 GCAGCAGCC 615
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RESULT 8
CB865829
LOCUS
DEFINITION CB865829 HD10N11w HD Hordeum vulgare cDNA clone HD10N11 3-PRIME, mRNA
sequence.
ACCESSION CB865829
VERSION CB865829.1 GI:30067805
KEYWORDS EST.
SOURCE
ORGANISM Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.
1 (bases 1 to 677)
Zhang, H., Weschke, W., Michalek, W., Stein, N. and Graner, A.
EST sequencing and analysis in barley (2002)
Unpublished (2002)
JOURNAL
COMMENT Contact: Stein Nils
Molecular Markers Group, Department Genbank
Institute of Plant Genetics and Crop Plant Research (IPK)
Corrensstr. 3, 06466, Gatersleben, Germany
Tel: 039482-5522
Fax: 039482-5595
Email: stein@ipk-gatersleben.de
Insert Length: 677 Std Error: 0.00
plate: 10 row: N column: 11
Seq primer: T7.
Location/Qualifiers
1. .677
source
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/organism="Hordeum vulgare"
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/db_xref="taxon:4513"
/clone="HD10N11"
/tissue_type="callus"
/dev_stage="callus (5-10 mm in diameter)"
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/clone_lib="HD"
/notes="Vector: pBluescript SK+; Site 1: EcoRI (5'-end of cDNA); Site 2: XhoI (3'-end of cDNA); Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRI adapter used for cloning. To excise the insert, restriction sites upstream EcoRI should be used (e.g. BamHI, SalI, PstI). NOTE: Also due to the cloning system used Blue/white selection for recombinants is not 100% reliable. Average insert size is 1 kb"

ORIGIN
Query Match 11.3%; Score 544.2; DB 14; Length 677;
Best Local Similarity 99.5%; Pred. No. 7.8e-114;
Matches 546; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 667 CGCATCAGGCGCTTTCGCTTCTCGCTCAGTCTCGCTCGCTCGCTCGCTCGCTCGCTG 726
|||
Db 68 CGTATTGGGCGCTTTCGCTTCTCGCTCAGTCTCGCTCGCTCGCTCGCTCGCTCGCTG 127
|||
QY 727 CGCGGAGCGGTATCAGTCTACTCANAAGGCGGTAAATACGGTTATCCACAGAAATCAGGGAT 786
|||
Db 128 CGCGGAGCGGTATCAGTCTACTCANAAGGCGGTAAATACGGTTATCCACAGAAATCAGGGAT 187
|||
QY 787 AACCCAGGAAAGAACATGTGAGCAAAAGGCGCAGCAAAAGGCCAGGAACCCGTAAAGAGGCC 846
|||
Db 188 AACCCAGGAAAGAACATGTGAGCAAAAGGCGCAGCAAAAGGCCAGGAACCCGTAAAGAGGCC 247
|||
QY 847 GCCTTGTGCGCTTTTTCATAGGCTCCGCCGCCCTGACGAGCATCAAAAATTCGACGC 906
|||
Db 248 GCCTTGTGCGCTTTTTCATAGGCTCCGCCGCCCTGACGAGCATCAAAAATTCGACGC 307
|||
QY 907 TCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAGATACCAAGGCTTCCGCCCTGA 966
|||
Db 308 TCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAGATACCAAGGCTTCCGCCCTGA 367
|||
QY 967 AGCTCCCTCGTGGCTCTCTGTTCCGACCTCGCGCTTACCGGATACCTGTCCGCCCTTT 1026
|||
Db 368 AGCTCCCTCGTGGCTCTCTGTTCCGACCTCGCGCTTACCGGATACCTGTCCGCCCTTT 427
|||
QY 1027 CTCCTTTCCGGAAGCGTGGCGCTTTTCATAGTCAAGCTGTAGTATTCAGTTCGGTG 1086
|||
Db 428 CTCCTTTCCGGAAGCGTGGCGCTTTTCATAGTCAAGCTGTAGTATTCAGTTCGGTG 487
|||
QY 1087 TAGGTCTGCTCCAAAGCTGGGCTGTGTGCAAGAACCCCGCTTACGCCGAGCCGCTGC 1146
|||
Db 488 TAGGTCTGCTCCAAAGCTGGGCTGTGTGCAAGAACCCCGCTTACGCCGAGCCGCTGC 547
|||
QY 1147 GCCTTATCCGGTAAGTATCTGTTAGTCCAAACCCGCTTAAGACACGACTTATCGCCACTG 1206
|||
Db 548 GCCTTATCCGGTAAGTATCTGTTAGTCCAAACCCGCTTAAGACACGACTTATCGCCACTG 607
|||
QY 1207 GCAGCAGCC 1215
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Db 608 GCAGCAGCC 616
|||
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RESULT 9
BQ660140
LOCUS
DEFINITION BQ660140 HI Hordeum vulgare subsp. vulgare cDNA clone HI01C11
3-PRIME, mRNA sequence.
ACCESSION BQ660140
VERSION BQ660140.1 GI:21801273
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QY 727 CGCGAGCGGTATCAGCTCACTCAAGCGGTATACGGTTATCCACAGAAATCAGGGAT 786
Db 131 CGCGAGCGGTATCAGCTCACTCAAGCGGTATACGGTTATCCACAGAAATCAGGGAT 190
QY 787 AACCGAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAAACCGTAAAAAGGCC 846
Db 191 AACCGAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAAACCGTAAAAAGGCC 250
QY 847 GCGTTGCTGCGGTTTTTCCATAGGCTCGGCCCGCCCTGACGAGCATCAAAAATTCAGCGC 906
Db 251 GCGTTGCTGCGGTTTTTCCATAGGCTCGGCCCGCCCTGACGAGCATCAAAAATTCAGCGC 310
QY 907 TCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAGATACAGGGGTTTTCCCGCTGGA 966
Db 311 TCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAGATACAGGGGTTTTCCCGCTGGA 370
QY 967 AGCTCCCTCGTGGGCTCTCTGTTTCCGACCGCTGCGGCTTACCGGATACCTGTCCGCGTTT 1026
Db 371 AGCTCCCTCGTGGGCTCTCTGTTTCCGACCGCTGCGGCTTACCGGATACCTGTCCGCGTTT 430
QY 1027 CTCCCTTCGGAGAGCGTGGGCTTTCTCATAGCTCAGCTGTAGGTATCTCAGTTCCGGTG 1086
Db 431 CTCCCTTCGGAGAGCGTGGGCTTTCTCATAGCTCAGCTGTAGGTATCTCAGTTCCGGTG 490
QY 1087 TAGTGCTTCGCTCCAGCTGGGCTGTGACGAAACCCCGTTACGCGCCGACCGCTGC 1146
Db 491 TAGTGCTTCGCTCCAGCTGGGCTGTGACGAAACCCCGTTACGCGCCGACCGCTGC 550
QY 1147 GCCTTATCCGGTAACTATCGTCTTGTAGTCCAAACCGGTAAAGACACGACTTATCGCCACTG 1206
Db 551 GCCTTATCCGGTAACTATCGTCTTGTAGTCCAAACCGGTAAAGACACGACTTATCGCCACTG 610
QY 1207 GCAGCAGCC 1215
Db 611 GCAGCAGCC 619

RESULT 11
AJ281437
LOCUS
DEFINITION
4A3A-P4C3-F Anopheles gambiae immune competent 4A3A Anopheles
gambiae cDNA clone 4A3A-P4C3, mRNA sequence.
ACCESSION
AJ281437
VERSION
AJ281437.1 GI:6929317
KEYWORDS
EST.
SOURCE
Anopheles gambiae (African malaria mosquito)
ORGANISM
Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
Anopheles.
1. (bases 1 to 703)
Dimopoulos, G., Casavant, T.L., Chang, S., Scheetz, T., Roberts, C.,
Donohue, M., Schultz, J., Benes, V., Bork, P., Ansorge, W., Soares, M.B.
and Kafatos, F.C.
Anopheles gambiae pilot gene discovery project: identification of
mosquito innate immunity genes from expressed sequence tags
Generated from immune-competent cell lines
Proc. Natl. Acad. Sci. U.S.A. 97 (12), 6619-6624 (2000)
20300950
MEDLINE
PUBMED
10841561
COMMENT
Contact: Dimopoulos G
Fotis C. Kafatos laboratory
European Molecular Biology Laboratory
Meyerhofstrasse 1, 69117 Heidelberg, Germany.
Location/Qualifiers
1. 703
/organism="Anopheles gambiae"
/mol_type="mRNA"
/strain="4a r/r"
/db_xref="taxon:7165"
/clone="4A3A-P4C3"
/cell_line="immune competent 4A3A"
/lab_host="E. coli DH10B"

FEATURES
source
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ORIGIN
Query Match 11.3%; Score 544.2; DB 9; Length 703;
Best Local Similarity 99.5%; Pred. NO. 8e-114;
Matches 546; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 667 CGATCAGGGCTCTTCCGCTTCCTCGCTCAGTACTCGTGGCTCGGTCGTTCCGGCTG 726
Db 64 CGTATTGGGGCTCTTCCGCTTCCTCGCTCAGTACTCGTGGCTCGGTCGTTCCGGCTG 123
QY 727 CGCGAGCGGTATCAGCTCACTCAAGCGGTAAATACGGTTATCCACAGAAATCAGGGAT 786
Db 124 CGCGAGCGGTATCAGCTCACTCAAGCGGTAAATACGGTTATCCACAGAAATCAGGGAT 183
QY 787 AACCGAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAAACCGTAAAAAGGCC 846
Db 184 AACCGAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAAACCGTAAAAAGGCC 243
QY 847 GCGTTGCTGCGGTTTTTCCATAGGCTCGGCCCGCCCTGACGAGCATCAAAAATTCAGCGC 906
Db 244 GCGTTGCTGCGGTTTTTCCATAGGCTCGGCCCGCCCTGACGAGCATCAAAAATTCAGCGC 303
QY 907 TCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAGATACAGGGGTTTTCCCGCTGGA 966
Db 304 TCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAGATACAGGGGTTTTCCCGCTGGA 363
QY 967 AGCTCCCTCGTGGGCTCTCTGTTTCCGACCGCTGCGGCTTACCGGATACCTGTCCGCGTTT 1026
Db 364 AGCTCCCTCGTGGGCTCTCTGTTTCCGACCGCTTACCGGATACCTGTCCGCGTTT 423
QY 1027 CTCCCTTCGGAGAGCGTGGGCTTTCTCATAGCTCAGCTGTAGGTATCTCAGTTCCGGTG 1086
Db 424 CTCCCTTCGGAGAGCGTGGGCTTTCTCATAGCTCAGCTGTAGGTATCTCAGTTCCGGTG 483
QY 1087 TAGTGCTTCGCTCCAGCTGGGCTGTGACGAAACCCCGTTACGCGCCGACCGCTGC 1146
Db 484 TAGTGCTTCGCTCCAGCTGGGCTGTGACGAAACCCCGTTACGCGCCGACCGCTGC 543
QY 1147 GCCTTATCCGGTAACTATCGTCTTGTAGTCCAAACCGGTAAAGACACGACTTATCGCCACTG 1206
Db 544 GCCTTATCCGGTAACTATCGTCTTGTAGTCCAAACCGGTAAAGACACGACTTATCGCCACTG 603
QY 1207 GCAGCAGCC 1215
Db 604 GCAGCAGCC 612

RESULT 12
CF752100
LOCUS
DEFINITION
TGDR9 Human thyroid of Graves disease Subtractive Library Homo
sapiens cDNA, mRNA sequence.
ACCESSION
CF752100
VERSION
CF752100.1 GI:37659538
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1. (bases 1 to 863)
Wen, G.-B., Wen, R. and Zhou, Y.
Screening and Cloning differentially expressed genes of Graves
disease by Suppression Subtractive Hybridization
Unpublished (2003)
JOURNAL
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Qy 1147 GCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAGACACGACTTATCGCCACTG 1206

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Qy	667	CGCATCAGGCGCTTTCCGCTTCTCGCTCACTGACTCGCTCGCTCGCTCGTTCGGCTG	726
Db	306	CGTATTGGGCGCTTCTCGCTTCTCGCTCACTGACTCGCTCGCTCGTTCGGCTG	365
Qy	727	CGGCGAGCGGTATCAGTCACTCAAGGCGGTATACGGTTATCCACAGAAATCAGGGAT	786
Db	366	CGGCGAGCGGTATCAGTCACTCAAGGCGGTATACGGTTATCCACAGAAATCAGGGAT	425
Qy	787	AACGCGAGAAAGAACATGTGAGCAAAAGGCCAGCAAGGCCAGGAACCGTAAAGAGGCC	846
Db	426	AACGCGAGAAAGAACATGTGAGCAAAAGGCCAGCAAGGCCAGGAACCGTAAAGAGGCC	485
Qy	847	GCCTTGTGCGGTTTTTCCATAGGCTCCGCCCTGACGAGCATCAAAAAATCGACGC	906
Db	486	GCCTTGTGCGGTTTTTCCATAGGCTCCGCCCTGACGAGCATCAAAAAATCGACGC	545
Qy	907	TCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAGATACAGGGGTTTCCGCTTGA	966
Db	546	TCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAGATACAGGGGTTTCCGCTTGA	605
Qy	967	AGCTCCCTCGTGGCTCTCTGTTCCGACCTGCGGCTTACCGGATACCTGTCCGCTTT	1026
Db	606	AGCTCCCTCGTGGCTCTCTGTTCCGACCTGCGGCTTACCGGATACCTGTCCGCTTT	665
Qy	1027	CTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCAGCTGTAGGTATCTCAGTTCGGTG	1086
Db	666	CTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCAGCTGTAGGTATCTCAGTTCGGTG	725
Qy	1087	TAGGTGCTTCGCTCCAGCTGGGCTGTGTGACGACCCCGCTTACGCCGACCGCTGC	1146
Db	726	TAGGTGCTTCGCTCCAGCTGGGCTGTGTGACGACCCCGCTTACGCCGACCGCTGC	785
Qy	1147	GCCTTATCCGTTAACTATGCTTTGAGTCCAAACCGGTAAAGACAGCACTTATCGCCACTG	1206
Db	786	GCCTTATCCGTTAACTATGCTTTGAGTCCAAACCGGTAAAGACAGCACTTATCGCCACTG	845
Qy	1207	GCAGCAGCC	1215
Db	846	GCAGCAGCC	854

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